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NY-LU-12   KEHSPPPPKVVHPLIGLLGEYGGDSDYEEEEEEEQTPPPQPRTAQPQKREEQTKKENEEDKLTDWNKLACLLCRRQFPNKEVL 970
LUCA15     PELVRNGDEEHPLKRGLVAAYSGDSDNEE....................ELVERLESEEEKLADWKKMACLLCRRQFPNKDAL 662
DXS8237E   DLPKLASDDRPSPPRGLVAAYSGESDSEE....................EQERGGPEREEKLTDWQKLACLLCRRQFPSKEAL 233

NY-LU-12   TIHQQLSDLPKQHLEIHRKIKQSEQELAYLERRERE.GKFKGRGNDRREKLQSFDSPERKRIKYSRETDS..DRKLVDKEDID 1050
LUCA15     VRHQQLSDLHKQNMDIYRRSRLSEQELEALELREKE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQPTKDGID 742
DXS8237E....TEHQQLSGLHKQNLEIHRRAHLSENELEALEKNIEMEQNKYRDRAAERREKYGIPEPPEPKRRKYGGISTASVDFEQPTKDGLC 316

NY-LU-12   TISKGLGVQQATGHRKGTGLGYKHPGLASSHEAEGRHRGPSVGASGRTSKRQSHETYRDAVRRVMFARYKELD      1123
LUCA15     HGNIGNKMLQAMGWREGSGLGRKKQGITAPIEAQVRLKGAGLGAKGSAYGLSGADSYKDAVRKAMFARFTEME      815
DXS8237E   SINIGSKMLQAMGWKEGSGLGRKKQGIVTPIEAQTRVRGSGLGARGSSYGVTSTESYKETLHKTMVTRFNEAQ      389
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(57) Abstract

Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.

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CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

Field of the Invention

The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with breast cancer. The invention also relates to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules, polypeptides coded for by such molecules and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic contexts.

Background of the Invention

The mechanism by which T cells recognize foreign materials has been implicated in cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been described. In many instances, the antigens recognized by these clones have been characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL clones which recognize the antigen-expressing cells can be isolated and propagated. While this approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera are used to identify immunogenic protein antigens expressed in cancer cells by screening expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified have been found to have elicited an high-titer humoral immune response in the patients from which the antisera were obtained. Such a high-titer IgG response implies helper T cell recognition of the detected antigen. These tumor antigens can then be screened for the presence of MHC/HLA class I and class II motifs and reactivity with CTLs

The invention is elaborated upon in the disclosure which follows.

Summary f the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer. Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) and agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter .composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

In one embodiment the sequence of contiguous nucleotides is selected from the group consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical to the sequence Group 1.

In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides and every integer length therebetween.

In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent,

which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein. The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (I) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

Detailed Description of the Invention

In the above summary and in the ensuing description, lists of sequences are provided. The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not know that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

"Nucleic Acid Sequences"

NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by a an autologous antibody or lymphocyte.

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

PP Group 2. Polypeptides encoded by NA Group 2

PP Group 3. Polypeptides encoded by NA Group 3.

PP Group 4. Polypeptides encoded by NA Group 4.

PP Group 5. Polypeptides encoded by NA Group 5.

PP Group 6. Polypeptides encoded by NA Group 6.

PP Group 7. Polypeptides encoded by NA Group 7.

PP Group 8. Polypeptides encoded by NA Group 8.

PP Group 9. Polypeptides encoded by NA Group 9.

PP Group 10. Polypeptides encoded by NA Group 10.

PP Group 11. Polypeptides encoded by NA Group 11.

PP Group 12. Polypeptides encoded by NA Group 12.

PP Group 13. Polypeptides encoded by NA Group 13.

PP Group 14. Polypeptides encoded by NA Group 14.

PP Group 15. Polypeptides encoded by NA Group 15.

PP Group 16. Polypeptides encoded by NA Group 16.

PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH_2PO_4(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to

manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (ftp:/ncbi.nlm.nih.gov/pub/). Exemplary tools include the BLAST system available at http://wwww.ncbi.nlm.nih.gov. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained using the MacVetor sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674. The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.*, Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990).for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below). Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

Immunol. 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term

"pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., ß-galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined

when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1α, which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e, the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant

negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an $F(ab')_2$ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for $F(ab')_2$, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

human or non-human sequences; chimeric $F(ab')_2$ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technitium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon-α, lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include $CD34^+$ hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2-

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio or 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-1410,1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114,1991) exemplifies this approach, showing the use of transfected cells expressing HPVE7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 μg to about 100 μg. Other adjuvants are known in the art and can be used in the invention (*see, e.g.* Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. I mmunol,* 154:5637-5648 (1995). Tumor cell transfection with B7 has ben discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., J Immunol, 19:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.,* 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther,* 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Fenton et al., *J. Immunothera*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS, Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 7:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venzuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Cliffton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-$CaPO_4$ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule. Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

When administered, the therapeutic compositions of the present invention can be

administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 μg, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen of variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (*see, e.g.* Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as

capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono-or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

Examples

Example 1: Preparation of breast cancer cDNA expression libraries

Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

A Dynabeads mRNA isolation kit (Dynal, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTT-Xba 1 site

Step 4: Ligation into the TriplEx vector arms.

The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

Step 6: Titering and amplification of generated libraries was performed accoding to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene) according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	1.8×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	3.5×10^6 pfu	Invasive Ductal Carcinoma,Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopoathological diagnosis
HBR173	2.3×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	1.1×10^6 pfu	Ivasive Ductal Carcinoma, Grade II
HBR257	2.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR297	4.0×10^6 pfu	Ductal Carcinoma, Grade II
HBR248	1.0×10^6 pfu	Invasive Ductal Carcinoma with Vascular Permeation,Grade III

HBR271	2.5 x 10^6 pfu	Medullary Carcimoma
HBR263	10.0 x 10^6 pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No serum-positive clones were found by screening HBR271 library.

Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at - 70°C prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDM) and stored at 4°C. Library screening was performed as described by Sahin et al.(*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4 x 10^3 per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at 37°C. Membranes were then blocked with 5% NFDM. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3' diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium chloride/5-bromo-4-chloro- 3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of 5 x 10^5 recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

Example 3: DNA Sequencing

Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
LONY-Br-1	L34543	LONY-Br-23	AA262134, U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT- PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 μg poly A^+ RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed ^{32}P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of $2.5x10^6$, $1.1x10^6$, and $1.7x10^6$ cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of huma antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'diamino benzidine tetrachloride, and 0.015% H_2O_2, in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na_3N. The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five time. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this

work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOs:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro-α collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOs:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

Example 7:Isolation and analysis of colon clones

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A^+ RNA, using commercially available products designed for this purpose.

The poly A^+ RNA was then converted into cDNA, and ligated into λZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g.*, Ace et al, *Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into λZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had E. coli Y1090 lysates coupled thereto, and then lysates from bacteriophage infected E. coli BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of 4×10^3 phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described supra. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-. Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA$^+$ RNA were analyzed from these samples, using random, ^{32}P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 68°C, for 30 minutes each time.

SEQ ID NOs:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

It is reported above that fourteen clones reacted with subsets of serum from both normal

and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophillins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosymal protein. The molecule set forth in SEQ ID NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with Drosophila homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
580	2/16	2/16
582	2/16	3/16
584	2/16	2/16
586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

Table 8: RT-PCR analysis of colon SEREX clones

normal tissue	SEQ ID NO.:550	SEQ ID NO.:552	SEQ ID NO.:558	SEQ ID NO.:560
kidney	+	Negative	Negative	Negative
colon	+	Negative	Negative	Negative
small		Negative	Negative	Negative
intest.	+	Negative	Negative	Negative
brain	+	Negative	Negative	Negative
stomach	+	Negative	Negative	Negative
testis	+	Negative	Negative	Negative
pancreas	+	Negative	Negative	Negative
lung	+	Negative	Negative	Negative
liver	+	Negative	Negative	Negative
heart	+	Negative	Negative	Negative
fetal		Negative	Negative	Negative
brain	+	Negative	Negative	Negative
mammary		Negative	Negative	Negative
gland	+	Negative	Negative	Negative
bladder	+	Negative	Negative	Negative
adrenal		Negative	Negative	Negative
gland	+	Negative	Negative	Negative
uterus	Negative	Negative	Negative	Negative
skeletal		Negative	Negative	Negative
muscle	Negative	Negative	Negative	Negative
PBL	Negative	Negative	Negative	Negative
placenta	Negative	Negative	Negative	Negative

spleen	Negative	Negative	Negative	Negative
thymus	Negative	Negative	Negative	Negative
esophagus	Negative	Negative	Negative	Negative
<u>Tumor Tissue</u>				
renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
colon primary tumors (10)	+ (10/10)	+ (10/10)	+(10/10)	Negative
colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
breast cancer (6)	+ (3/6)	Negative	Negative	Negative
lung cancer (6)	+ (6/6)	Negative	Negative	Negative
gastric cancer (1)	+	+	+	Not tested
<u>colon cancer cell lines</u>				
colo 205	+	+	+	Negative
HT29	+	+	Negative	Negative
HCT15	Negative	Negative	Negative	Negative

<u>Example 8:Isolation and analysis of additional clones</u>

For the establishment of a cDNA library from human tissue total RNA was obtained from 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into λZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library resulted in 1.8 x 10^6 recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was 10^{11} plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.

In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic λ phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

E. coli bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of $OD_{600} = 1.0$, the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with 10^6 λZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of $4\text{-}5 \times 10^3$ plaque forming units (pfu) per plate in LB-medium with isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made in possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of 1.8×10^6 recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by in vivo excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the λZAPII phage vectors and used for the transfection of E. coli SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Norther blot analysis demonstrated that the mRNA of clone HOM-

RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above, allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme EcoR1, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into E. coli of strain BL21 as described (Spindleret al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with E. coli and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum. Reactivity was detected at dilutions of 1: >100,000.

Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of $8x10^5$ clones were screened with autologous serum, and $4.5x10^3$ clones were screened with three different allogeneic sera. Twenty three clones, representing seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocelullar carcinoma libraries were studied in the same way, a total of $1.5x10^6$ clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galactin-9 was expressed only in a small, subpopulation of dendritic cells.

Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microlubules. It was found that both resin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microlubile systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 mengioma tumor samples were found to express the gene.

Example 9:Isolation and analysis of lung cancer clones

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a λZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc γ secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an a ^{32}P-labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5'end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Dracopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 µl RT product in a final volume of 25 µl, with 2µCi of α^{32}P-dCTP (~3000 Ci/mmole, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 µl of the mixture was diluted with 5 µl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

Identification of Immunoreactive cDNA clones

A cDNA expression library of $1.42x10^7$ primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and $8x10^5$ phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-biding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin 1X [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin 1X are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsA component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.

et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identify with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on *TSG* locus of chromosome 3p21.

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the *TSG* locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996))]. Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies. The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length. An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

Additional cDNA variants of NY-LU-12

In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

<u>Features of NY-LU-12 and its putative gene product</u>

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3'end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition. This possibility was explored using DNA sequencing and single-strand confirmational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)

Table 10: RT-PCR analysis

Normal Tissue	BRDT	H1T
mammary gland	-	-
liver	-	-
small intestine	-	-
brain	-	+/- (very weak)
lung	-	-
fetal brain	-	-
placenta	+	+
kidney	-	-
skeletal muscle	-	-
pancreas	-	-
adrenal gland	-	-
heart	-	-
thymus	-	-
uterus	-	-
prostate	-	+/- (very weak)
spleen	-	-
Testis	+	+

Tumor Tissue	BRDT	H1T
Colon	0/6	0/6
Breast	0/6	6/6+
Melanoma	0/12	3/12+
Lung	8/26+	4/26+
Renal	0/2	0/2
Ovary	0/2	0/2
Esophageal	0/1	0/1

Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

Example 11: allogeneic serotyping

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules. CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and baceteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients

Sequence Gene/Clone	Number	Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
RPB-J H-2K binding factor		SM1	6/12	6/16
Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
Sterol carrier protein X		SM1	2/12	0/16
Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
M phase phophoprotein I		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16

FKBP25		KM, SS1	5/12	0/16
Pros-27		KM, CK	3/12	1/16
BS4		KM	1/12	1/16
GnRH-II		KM	1/12	0/16
CTBP		KM	1/12	0/16
ETF		KM	3/12	1/16
KIAA0438		KM	1/12	5/16
KIAA0367		KM	4/12	3/16
APK1		KM	2/12	0/16
IPP		KM	1/12	0/16
Tropomyosin		KM	1/12	0/16
p63		KM	1/12	0/16
KIAA0181		KM	1/12	0/16
KIAA0349		KM	1/12	0/16
RPB1		KM	5/12	9/15
PPIM		KM	1/12	-
EB virus		KM	3/12	-
G.KM073		KM	6/12	-
G.KM403		KM	1/12	-
KM192		KM	1/12	-
KM294		KM	1/12	-
KM362		KM	1/12	-
KM031		KM	1/12	-
KM081		KM	3/12	-
KM201		KM	1/12	-
KM1496		KM	1/12	-
KM334		KM	1/12	-
KM313		KM	1/12	
E-cad/Y		CK	1/12	0/16
IPBP		SS1	1/4	-
OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-

The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

Example 12: Preparation of recombinant cancer associated antigens

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 13: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 14: Expression of cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

Example 15: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (*see, e.g.,* Parker et al, *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL http://bimas.dcrt.nih.gov. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

Table 12: Identification of HLA binding peptides in lung SEREX clones

HLA	peptide	amino acids of NY-LU-12 protein	SEQ ID NO
A1	NVEE-HSFSY	67 - 75	713
	PVDP-NILDY	287 - 295	714
	DTDY-RSMEY	398 - 406	715
A2	SLLE-DAIGC	506 - 514	716
	TLMI-QDKEV	521 - 529	717
	YVSSLDFWYC	533 - 542	718
	VIVEVLEPYV	671 - 680	719
	KLTD-WNKLA	948 - 956	720
	QLSDLHKQNL	975 - 984	721
	KQSEQELAYL	991 - 1000	722
	KLVDKEDIDT	1042 - 1051	723
	VMFA-RYKEL	1114 - 1122	724
A3	QMFG-YGQSK	417 - 425	725
	GMPVKNLQLK	481 - 490	726
	GLPE-EEEIK	823 - 831	727
	LLCRRQFPNK	958 - 967	728
A24	EYRD-VDHRL	405 - 413	729
	GYVC-VEFSL	499 - 507	730
	DYGY-VCVEF	497 - 505	731
	WYCKRCKANI	540 - 549	732
	TYPQPQKTSI	574 - 583	733
	IYRSTPPEVI	663 - 672	734
	HYYQ-GKKYF	754 - 762	735
	VYVP-QDPGL	816 - 824	736
B7	WNRDYPPPPL	26 - 35	737
	MPPV-DPNIL	285 - 293	738
	TARD-AQRDL	432 - 440	739
	GPSEEKPSRL	448 - 457	740
	TPPEVIVEVL	667 - 676	741
	RVMFARYKEL	1113 - 1122	742
B44	REMG-SCMEF	272 - 280	743
	EEQSSDAGLF	376 - 385	744
	KEYN-TGYDY	490 - 498	745
	TEAKQELITY	566 - 575	746
	VEALRVVKIL	710 - 719	747
	GEYG-GDSDY	906 - 914	748
	LERREREGKF	1000 - 1009	749

B52	RQDGESKTIM	650 - 659	750
	TPPEVIVEVL	667 - 676	751
	YGFIDLDSHV	701 - 710	752
	RQFP-NKEVL	962 - 970	753

NY-LU-12B (variant B)

A1	NVEE-HSFSY	121 - 129	754
	PVDP-NILDY	341 - 349	755
	DTDY-RSMEY	452 - 460	756
A2	WQSA-RFYYL	41 - 49	757
	SLLE-DAIGC	560 - 568	758
	TLMI-QDKEV	575 - 583	759
	YVSSLDFWYC	587 - 596	760
	VIVEVLEPYV	725 - 734	761
	KLTD-WNKLA	1002 - 1010	762
	QLSDLHKQNL	1029 - 1038	763
	KQSEQELAYL	1045 - 1054	764
	KLVDKEDIDT	1096 - 1105	765
	VMFA-RYKEL	1168 - 1176	766
A3	QMFG-YGQSK	471 - 479	767
	GMPVKNLQLK	535 - 544	768
	GLPE-EEEIK	877 - 885	769
	LLCRRQFPNK	1012 - 1021	770
A24	YYLN-ATDVL	47 - 55	771
	FYYLNATDVL	46 - 55	772
	EYRD-VDHRL	459 - 467	773
	GYVC-VEFSL	553 - 561	774
	DYGY-VCVEF	551 - 559	775
	WYCKRCKANI	594 - 603	776
	TYPQPQKTSI	628 - 637	777
	IYRSTPPEVI	717 - 726	778
	HYYQ-GKKYF	808 - 816	779
	VYVP-QDPGL	870 - 878	780
B7	WNRDYPPPPL	80 - 89	781
	MPPV-DPNIL	339 - 347	782
	TARD-AQRDL	486 - 494	783
	GPSEEKPSRL	502 - 511	784
	TPPEVIVEVL	721 - 730	785
	RVMFARYKEL	1167 - 1176	786

B44	SEAWSSNEKF	59 - 68	787
	REMG-SCMEF	326 - 334	788
	EEQSSDAGLF	430 - 439	789
	KEYN-TGYDY	544 - 552	790
	TEAKQELITY	620 - 629	791
	VEALRVVKIL	764 - 773	792
	GEYG-GDSDY	960 - 968	793
	LERREREGKF	1054 - 1063	794
B52	RQDGESKTIM	704 - 713	795
	TPPEVIVEVL	721 - 730	796
	YGFIDLDSHV	755 - 764	797
	RQFP-NKEVL	1016 - 1024	798

Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen

To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see*, e.g., Knuth et al., *Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.*24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230, 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ^{51}Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ^{51}Cr release as above.

Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references disclosed herein are incorporated by reference in their entirety.

We claim:

TABLE 1

SEQ ID NO. 1:

U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

SEQ ID NO. 3:

X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

SEQ ID NO. 4:

AA900930, AA925665.

SEQ ID NO. 5:

U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, Z99290, M30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574,

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527, AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204, AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395, AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787, AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

SEQ ID NO. 7:

X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750, X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008, D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337, X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880, AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916, AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461, AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410, AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615, AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506, M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054, AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309, AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611, AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258, AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075, N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161, AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148, AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792, AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516, AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779, AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483, C64685, AA851367, C91730, AA143899, T23399.

SEQ ID NO. 9:

AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241, AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846, AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802, AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761, C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390, AA848674, AA924440, T15031, AA451569, H35524.

SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, A175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115, AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907.

SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619, Z45284, H14105, R84666, AA090321, AA350108, W52840, R48497, R13097, T66255, W44467, AA247676, AA198489, AA388175, AA261453, AA237111, AA790730, AA162394, AA816498, AI013729, AA684961, AA979759.

SEQ ID NO. 15:

AF069301, D10651, U11419, U11287, M91562, U90278, U72724, X57855, X79424, M16512, M64542, Z14152, AF016667, L01488, Z75955, AF024504, M13968, W67775, AA934587, AA617696, AA913577, AA628682, W74527, AA969876, AA995606, AA622402, AA027090, AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124, AA733183, T90909, Z25096, AA721771, AA115089, T49643, R00622, N93780, R00626, AA365494, T71475, N74066, AA027130, T83325, AA115569, AA658299, T55344, T83700, AA426250, AA393863, AA282967, R08138, AI000112, AA807574, AA077926, AA397527, W87761, AA243026, R56368, H16371, AA958697, AA003997, AA008542, AA036229, AA397074, AA250467, AA260498, AA968175, AA253686, AA727785, AI019478, AA474978, AA543461, AA990281, AA245791, AA617042, AA015355, AA983015, AA982200, AA120064, AA462778, AA242574, AA986993, AA986911, AA882490, AA223057, AA543989, W65528, AA848318, AA874979, AA800547, AA945302, AA140994, AA991110, AA851120.

SEQ ID NO. 16:

Z68106, X14199, M14872, Z63497, M31670, AC002123, Z63498, AA280070, AA215687, H93207, AA070367, W95534, AA682436, AA741066, AA173269, AA641255, AA215688, AA724798, N23259, AA442155, AA634563, AA074699, AA642322, AA861347, AA283655, AI002587, W95419, AA357042, AA761253, AA197191, T54480, AA133029, AA378991, AA114599, AA219925, AA174327, AA003800, C86661, AA990433, AA277014, AA445101, AA671205, AI036728, AA241221, AA213304, AI035350, W08919, W36663, AA061406, AA144736, AA240583, AI006563, AA980152, AA250075, AA088967, W17488, AA098269, W10200, AA543712, AA755434, AI012680, AA820868, AA949519, AA391130, AA202576, AA979150, AA012391, AA539472.

SEQ ID NO. 17:

J03592, M24103, AB009386, U44832, J02966, M24102, U27316, U10404, X70847, D12771, D12770, J02683, J03591, U27315, M76669, U39779, M13783, J04982, X74510, X61667, M57424, L78810, AC004000, Z75206, U68723, Z75207, AF009661, X53264, J03320, U66060, AB011800, M77194, AE000021, L07268, AE000936, U03115, AF009663, AA582128, AA916851, AA576667, AA915921, AA916853, N58735, AA428106, AA427849, AI024255, H69807, H11315, N36980, H69597, AA826334, W05080, N37044, AA385873, N48222, AA394173, AA837522, AI002511, AA292870, T96300, AA360716, AA379604, AA862844, AA430455, AA479859, AA133899, AA669954, H92542, AA095298, AA995794, AI003667,

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SEQ ID NO. 20:

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SEQ ID NO. 21:

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SEQ ID NO. 22:

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SEQ ID NO. 23:

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SEQ ID NO. 25:

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SEQ ID NO. 26:

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SEQ ID NO. 27:

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SEQ ID NO. 28:

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SEQ ID NO. 29:

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SEQ ID NO. 30:

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SEQ ID NO. 31:

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SEQ ID NO. 109:

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SEQ ID NO. 111:

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SEQ ID NO. 121:

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SEQ ID NO. 123:

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SEQ ID NO. 127:

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SEQ ID NO. 131:

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SEQ ID NO. 133:

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SEQ ID NO. 135:

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SEQ ID NO. 137:

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SEQ ID NO. 139:

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SEQ ID NO. 141:

S45630, AF007162, X95383, AF029793, M55534, X60351, S77138, S77142, S74229, X60352, M63170, M24906, M28638, J03849, M12016, M73741, U04320, M12014, M24092, L08078, S53164, U26661, M12015, M25770, U16124, X87114, D29960, X14789, X85205, M17247, U05569, U66584, M26142, U47921, U47922, V01219, X95382, AP000007, AE000869, AB009529, AF062537, D10457, S37449, X59541, AA742442, AA704135, AA211774, N35834, AA482745, AA211607, N28898.

SEQ ID NO. 143:

U78082, L78810, U14573, AC004068, U07561, M98511, AC004673, AA613346, AA953216, AA305926, H92800, R98218, AA629543, AA297666, AA302982, AA429481, AA126005, AA837225, AA856961, AA946848, F13749, AA847704, AA833896, AA621381, AA833875, AA459962, H22141, N73060, AA491955, H28477, AA224463, AA708753, AA152253, AI028510, AA483606, AA992126, T54783, AA715075, AA568204, AA715173, N64587, AA570740, AA984258, AA904211, H94979, AA085410, AA599352, AA488620, AA574442, AI049845, AA593471, AA393830, AA610509, AA297145, AA113272, AA835889, AA655005, AA689351, R93919, AA613761, AA550989, AA303054, H07953, AA713815, AA827490, AA865262, AA461308, H73550, AA657835, AA362349, H82679, AA378682, AA577755, AA663472, AA490602, AA857673, AA347114, AI049630, AA086150, AI017251, AA877992, AA084609, AI050760, AA808998, AA503258, AA613138, AA603156, AA513293, R97934, AA610233, AA654874, AA501867, AA604831, N22058, AA492114, T50676, AA757426, AA584482, AA789192, AI004591, T50694, AA862227, AA594145, AA728911, AA847499, AA159978, AA534204.

SEQ ID NO. 145:

Z69030, L42375, U37352, D26445, U38192, U38191, U37770, U38190, U37353, U59418, L76702.

SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873, L07874.

SEQ ID NO. 149:

U07158, X85784, AJ000541, U76832, L20821, AC003089, AC004504, AF049236, L40609, AF053765, L14677, Z94056, Z18277, AE001073, U85969, X79283, AJ223473, AA632339, AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836, AA642711, AA085920, W22275, D20744, UMGS017, AA487868, AA487869, AA085919, 682 AA833281, AA619252, C77541, AA691960, AA763615, AA164051, AA259589, AA060475, AA254185, AA666705, AA272597, AA152985, AI011416, AA850008, H33152, AA941811.

SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181, L12399.

SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651, AP000031, U67588, X03991, AC004660, AL010261, V01515, M86251, L29376, Z71417, L78442, U00921, AC004692, AC003698, AE000742, Z49128, Z73417, Z71418, AA424638, AA442084, AA805748, AA835489, AA713576, AA502343, AA765949, AA812332, AA831755, AA417718, AA776946, AA152295, AA731660, R48791, AA150237, N51650, N52616, N52586, AA533556, AA305755, AA760877, AA729913, AA731659, AA910594, AA904521, AA372550, R48898, N50390, R08712, H83343, AA417867, AA090407, AA009846, AA927286, AA678135, AI033148, AI041408, AA235113, AA398662, M62215, W27276, AA885767, AA460155, AA742433, R19908, AA040696, AA555240, AA043160, AA292844, R53160, AA536080, N70013, N35921, N70096, AA277029, AA560610, AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892, C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855, AI021808, AI009216, D68214, AA220863, D70434.

SEQ ID NO. 157:

U43195, U58512, U61266, D89493, U36909.

SEQ ID NO. 159:

AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390, AA479958, N20112, R86178, R97894, T64868, W68074, AA365195, AA928749, AI037069, AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136, AA561223, AA183703, AA647218, AA792208, W48100, D40621, AJ225487, AA294595,

02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

SEQ ID NO. 161:

K01546, AE000468, X95549, AC004014, Z81584, L19201, X94244, X06932, U39479, X13301, AC000386, U80847, X86737, U39478, AA883211, AA610050, AA774254, AA280736, AA926725, AA459300, N55370, AA233666, H90342, T66839, H91250, AA856968, R92873, AI034196, AI014787, AA910410, AA088535, AA230765, AA467238, AA397279, AA420226, AA396042, AA200070, AA165873, AA762534, AA067133, AA065429, AA185092, AA572057, AA111387, AA175824, AA881071, AA571692, AA104279, AA733670, AI008804, D86670, C67200, D41938, AA141467, D35894, AI001643, AA957220, T37355, T18792, D47809, W21723, AA898504, AA951903, AA661025, AA949796, AA990685, AA661449, AA948837, R04787, D16046, AA439636, AA246769, AA978829, D43523, T02021, AA803212, D22651, AA201227, AA694728, AA891643, D23309, AA820831, D41871, W21774, D16065.

SEQ ID NO. 163:

X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857, X07265, M36830, M30626, AA669137, AA725103, AA890496, AA314095, AA554815, AA313331, AA730100, AA214035, AA876412, AA121630, AA314010, AA927532, AA968674, AA679253, N66271, AA558907, AA309988, AA587079, AA075436, AA160964, AA205657, AA214083, AA130903, AA917032, AA149623, AA857523, AA889843, AA305037, AA491055, W73240, AA255644, W73295, AA765431, AA178947, N66409, AA074895, AA306976, AA075052, AA075387, AA130892, AA857443, AA405942, AA629891, AA152004, AA129550, W56527, AA513807, AA703828, AA223171, C75280, AA889155, AA854676, AA773063, AA774999, AA152392, AA307057, AA316954, AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299, AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763, AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942, N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908, AA699607, AA086423, N72134, AA630369, AA564649, AA046806, AA666249, AA306893, AA225404, AA127417, AA854951.

SEQ ID NO. 165:

M23885, AF047868, AF017732, AB005249, Z83229, AF026483, U97194, Z67884, Z67881, X13481, X07651, AC001226, AC002542, AB002307, AA984684, AA017533, AA306600, AA261957, F08123, R17885, AA282208, H85861, H85836, AA593150, H87276, AA057384, AA243602, AA013399, AA374926, AA721341, R88896, AA021538, AA101740, AA375314, AA090398, H86058, AA984556, AA215816, AA092672, AA034243, AA328017, F11174, AA261777, N40306, W21253, R02386, AA349225, AI038487, H98027, AA385878, AA075431, AA375596, R77638, T73214, AA310841, AA062331, AA919318, AA606883, 373 AA174568, AA790426, AA423321, AA647673, AA109549, AA396473, W16215, AA105538, AA061105, AA066766, AA462773, AA555644, AA499452, AA389523, AA245036, AA475340, AA880992, AA198965, W11981, AA509705, AA237414, AA646230, AA673569,

AA239037, AA672620, AA915168, AA863498, AA123378.

SEQ ID NO. 167:

Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

U33822, X61838, AA572230, AA589570, AA929790, AA104830, C81582, AA271190, AA290278, AA543616, AI043207, AA107832, AA958460, AI020992, AA795905, AA277468, AA475069, AA111610, AA389139, AA154163.

SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251, AA394101, N35855, N56791, N35444, AA147382, AA647547, AA939939, AA895989, AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625, AA033190, AA175922, AA172918, AA895209, AA028700, AA416048, AA175247, AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642, AA848690, AA800525, AA802510, C24001, AA841755, AA882663, D40069, AA433358, D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662, AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169, AA751535.

SEQ ID NO. 174:

Z81364, AC003033, AE000665, AA570483, AA532739, AA526905, AA725306, AA134415, AA651838, AA481316, AA600310, C04532, AA004615, H20713, AA913640.

_SEQ ID NO: 176

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SEQ ID NO: 177

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SEQ ID NO: 178

Z50194, U92983, U44088, AC003101, X72892, AF035444, M32474, AF019953, AC001228, Y15443, AF001294, U12418, X06956, M31176, AF015277, AF002708, R43556, AA088367, AA313553, H92530, AA376262, T09403, AA814143, R75643, AA479005, AA773048, AA507143, AA402127, AA430292, AI015600, AA393069, AA463606, AA885498, AA460759,

AA398766, R48359, AA426107, AA909990, AI017459, AA076224, N39533, AI026941, AA412699, AA292828, AI024759, AI016910, AA573306, R48386, AA065307, AA774549, AI016070, AA884918, AA431512, AA306051, AA476440, AA292924, AA621059, AA411830, AA405079, AA596171, AA989987, AA472637, AA690249, AA691927, AA792720, AA637983, AA020137, AA097337, AA117759, W17615, AA285526, AA111347, AA208823, AA879750, AA413058, W33316, AA161891, W41259, AA511152, AA027481, AA020252, AA033106, AA965045, D41048, AI031042, D48020, AA925258, D40853, AA945674, C19585, AI013412, T15040, AA541011, AA990782, AA851306, AA540938, T23386, AA783863, AA979035, AA951002, AA438957, AA979006, AA978995, AA800046, AA556128, C27411, D15562, T20348, AA966363, AA949269, AA785774, AA728671, D16092, N37869, D48782.

SEQ ID NO: 179

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SEQ ID NO: 180

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SEQ ID NO: 181

U52191, D87072, AL022162, AL008710, Z83850, AF055066, AC004254, L25270, AC003013, U53141, AL021728, AC004997, M38703, AC004020, U91321, AP000041, Z69921, AC002551, D87016, X54171, AF055481, X83213, L05489, AC003018, AB009056, AC000069, L81890, AD000685, AC003031, AC003030, Z99715, AF043301, AE000664, AF007544, X15547,

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SEQ ID NO: 322

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SEQ ID NO: 510

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SEQ ID NO: 511

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SEQ ID NO: 512

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SEQ ID NO: 513

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W52500, W52500 zd13d02.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
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AA057030, AA057030 zk78b03.r1 Soares pregnant uterus NbHPU Ho... 698 0.0
AA496417, AA496417 zv37b03.r1 Soares ovary tumor NbHOT Homo s... 686 0.0
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AA042995, AA042995 zk56b07.r1 Soares pregnant uterus NbHPU Ho... 668 0.0
H69274, H69274 EST00070 Homo sapiens cDNA clone HE6WCR117 5'. 658 0.0
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AA436368, AA436368 zv32f05.s1 Soares ovary tumor NbHOT Homo s... 585 e-165
AA975130, AA975130 on06f01.s1 NCI_CGAP_Lei2 Homo sapiens cDNA... 579 e-163
AA885226, AA885226 am34e06.s1 Soares NFL T GBC S1 Homo sapien... 559 e-157
AA912472, AA912472 ol96e03.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 555 e-156
AA320935, AA320935 EST23388 Adipose tissue, white II Homo sap... 553 e-155

AA042872, AA042872 zk56b07.s1 Soares pregnant uterus NbHPU Ho... 543 e-152
T08932, T08932 EST06824 Homo sapiens cDNA clone HIBBM46 5' end. 537 e-150
AA488258, AA488258 ad08f07.r1 Soares NbHFB Homo sapiens cDNA ... 533 e-149
T19350, T19350 h03012t Testis 1 Homo sapiens cDNA clone h0301... 496 e-138
H87681, H87681 yw15e04.r1 Homo sapiens cDNA clone 252318 5'. 490 e-136
H81522, H81522 yu61h08.r1 Homo sapiens cDNA clone 230655 5'. 466 e-129
T49620, T49620 ya77g03.s1 Homo sapiens cDNA clone 67732 3'. 452 e-125
R14363, R14363 yf80d10.r1 Homo sapiens cDNA clone 28995 5' si... 446 e-123
AA211476, AA211476 zp75h11.s1 Stratagene HeLa cell s3 937216 ... 430 e-118
N46636, N46636 yy48a09.r1 Homo sapiens cDNA clone 276760 5'. 424 e-116
Z17358, HSDHII065 H. sapiens partial cDNA sequence; clone HI... 416 e-114
R40737, R40737 yf80d10.s1 Homo sapiens cDNA clone 28995 3'. 400 e-109
AA410278, AA410278 zv32f05.r1 Soares ovary tumor NbHOT Homo s... 383 e-104
AA496574, AA496574 zv37b03.s1 Soares ovary tumor NbHOT Homo s... 375 e-101
N34907, N34907 yy48a09.s1 Homo sapiens cDNA clone 276760 3'. 371 e-100
T49619, T49619 ya77g03.r1 Homo sapiens cDNA clone 67732 5'. 355 1e-95
AA301480, AA301480 EST14551 Thymus III Homo sapiens cDNA 5' end 341 2e-91
R31593, R31593 yh76f03.s1 Homo sapiens cDNA clone 135677 3'. 317 2e-84
AA984591, AA984591 am89d10.s1 Stratagene schizo brain S11 Hom... 313 4e-83
AA338831, AA338831 EST43831 Fetal brain I Homo sapiens cDNA 5... 238 2e-60
T07305, T07305 EST05194 Homo sapiens cDNA clone HFBEG86. 230 4e-58
AA159942, AA159942 zo79c05.r1 Stratagene pancreas (#937208) H... 204 3e-50
R57355, R57355 F2878 Fetal heart Homo sapiens cDNA clone F287... 196 6e-48
AA729237, AA729237 nx35c08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 192 1e-46
AA877709, AA877709 nr09g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 172 9e-41
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AA584615, AA584615 no08g12.s1 NCI_CGAP_Phe1 Homo sapiens cDNA... 38 3.4
AA229827, AA229827 nc48c04.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 3.4
W21398, W21398 zb50a11.r1 Soares fetal lung NbHL19W Homo sapi... 38 3.4

AA136933, AA136933 zn97f07.s1 Stratagene fetal retina 937202 ... 38 3.4

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AA544727, AA544727 vk35d01.r1 Soares mouse mammary gland NbMM... 773 0.0
W84968, W84968 mf42e02.r1 Soares mouse embryo NbME13.5 14.5 M... 640 0.0
AA153324, AA153324 ms61e11.r1 Stratagene mouse embryonic carc... 617 e-175
AA673899, AA673899 vo86g07.r1 Barstead mouse irradiated colon... 583 e-164
AA797488, AA797488 vw28a05.r1 Soares mouse mammary gland NbMM... 519 e-145
W71831, W71831 me45b06.r1 Soares mouse embryo NbME13.5 14.5 M... 472 e-131
AA213358, AA213358 mu74e04.r1 Stratagene mouse embryonic carc... 444 e-123
W75918, W75918 me82f05.r1 Soares mouse embryo NbME13.5 14.5 M... 444 e-123
AA038141, AA038141 mi81e05.r1 Soares mouse p3NMF19.5 Mus musc... 359 3e-97
AA038288, AA038288 mi83b04.r1 Soares mouse p3NMF19.5 Mus musc... 323 1e-86
AA017742, AA017742 mh40c03.r1 Soares mouse placenta 4NbMP13.5... 297 8e-79
AA771297, AA771297 vt17g04.r1 Barstead mouse myotubes MPLRB5 ... 297 8e-79
AA105228, AA105228 mp45b11.r1 Barstead MPLRB1 Mus musculus cD... 295 3e-78
AA068340, AA068340 mm53f01.r1 Stratagene mouse embryonic carc... 293 1e-77
AA612347, AA612347 vo05c08.r1 Stratagene mouse skin (#937313)... 281 5e-74
AA038300, AA038300 mi83d04.r1 Soares mouse p3NMF19.5 Mus musc... 270 2e-70
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AA064466, AA064466 ml49c05.r1 Stratagene mouse testis (#93730... 107 2e-21
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AA120433, AA120433 mp82h11.r1 Soares 2NbMT Mus musculus cDNA ... 42 0.078
W08185, W08185 mb42h02.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.2
AA065563, AA065563 ml71b06.r1 Stratagene mouse kidney (#93731... 38 1.2
AA288756, AA288756 mr46h07.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA119334, AA119334 mp80e10.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA163051, AA163051 ms24a10.r1 Stratagene mouse skin (#937313)... 38 1.2
N28074, N28074 MDB1392R Mouse brain, Stratagene Mus musculus ... 38 1.2
AA288757, AA288757 mr46h08.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA122857, AA122857 mq06a02.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA617519, AA617519 vj77d05.r1 Knowles Solter mouse blastocyst... 38 1.2

W89420, W89420 mf80b03.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
AI047837, AI047837 ud64c11.x1 Sugano mouse liver mlia Mus mus... 38 1.2
AA840310, AA840310 vw91a10.r1 Stratagene mouse skin (#937313)... 36 4.8
AA986428, AA986428 ue13b04.x1 Sugano mouse embryo mewa Mus mu... 36 4.8
W47677, W47677 mc89g07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA057996, AA057996 mj56c10.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA183858, AA183858 mo95h01.r1 Stratagene mouse testis (#93730... 36 4.8
AA212232, AA212232 mu43e08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
W41067, W41067 mc39a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.8
AA967594, AA967594 uh01d06.r1 Soares mouse hypothalamus NMHy ... 36 4.8
AA414093, AA414093 vc64c07.s1 Knowles Solter mouse 2 cell Mus... 36 4.8
AA123833, AA123833 mp93c03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA432920, AA432920 vd91b11.r1 Soares mouse NbMH Mus musculus ... 36 4.8
AA874496, AA874496 vx03a08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA000433, AA000433 me76e09.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA023983, AA023983 mh94a07.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
AA013726, AA013726 mh12e09.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
AA274648, AA274648 vb08c01.r1 Soares mouse NML Mus musculus c... 36 4.8
AA140347, AA140347 mq89g06.r1 Stratagene mouse heart (#937316... 36 4.8
AA499377, AA499377 vi89c07.r1 Stratagene mouse heart (#937316... 36 4.8
C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8
AA726125, AA726125 vu88c06.r1 Stratagene mouse skin (#937313)... 36 4.8
AA760311, AA760311 vv71c12.r1 Stratagene mouse skin (#937313)... 36 4.8
AA763007, AA763007 vw60b05.r1 Soares mouse mammary gland NMLM... 36 4.8
AA929878, AA929878 vz44d03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
W59064, W59064 md67e10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA103519, AA103519 mo24b12.r1 Life Tech mouse embryo 13 5dpc ... 36 4.8
AA222310, AA222310 my14d08.r1 Barstead mouse heart MPLRB3 Mus... 36 4.8
W83557, W83557 mf32d02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA168631, AA168631 ms33c05.r1 Stratagene mouse skin (#937313)... 36 4.8
AA960143, AA960143 vw60b05.s1 Soares mouse mammary gland NMLM... 36 4.8
W34557, W34557 mc58a05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
W98818, W98818 mf94e06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA008527, AA008527 mg85h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA008734, AA008734 mg86h03.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA510568, AA510568 vg33a10.r1 Soares mouse mammary gland NbMM... 36 4.8
AA672524, AA672524 vo59e11.r1 Soares mouse mammary gland NbMM... 36 4.8
AA052773, AA052773 mf24h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA096626, AA096626 mo09h06.r1 Life Tech mouse embryo 10 5dpc ... 36 4.8
AA124880, AA124880 mp73e06.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA198005, AA198005 mv12b09.r1 GuayWoodford Beier mouse kidney... 36 4.8
AA624213, AA624213 vm98h06.r1 Knowles Solter mouse blastocyst... 36 4.8
AA521863, AA521863 vi08b01.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
AA692113, AA692113 vt19d03.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
W71551, W71551 me39e11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8

AA646501, AA646501 vn12g12.r1 Stratagene mouse heart (#937316... 36 4.8
AA607056, AA607056 vm95e05.r1 Knowles Solter mouse blastocyst... 36 4.8
AA163340, AA163340 ms65b10.r1 Stratagene mouse embryonic carc... 36 4.8
AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

AI030290, AI030290 UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor... 293 1e-77
C71833, C71833 Rice cDNA, partial sequence (E0428_1A) 44 0.017
AA926551, AA926551 TENS1173 T. cruzi epimastigote normalized ... 42 0.069
AA875699, AA875699 TENU0170 T.cruzi epimastigote normalized c... 42 0.069
AA567661, AA567661 HL01595.5prime HL Drosophila melanogaster ... 40 0.27
C74504, C74504 Rice cDNA, partial sequence (E31753_1A) 40 0.27
AA698333, AA698333 HL04291.5prime HL Drosophila melanogaster ... 38 1.1
AA441429, AA441429 LD16359.5prime LD Drosophila melanogaster ... 38 1.1
N68770, N68770 TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 1.1
AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1
AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1
N69148, N69148 TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 1.1
AA536484, AA536484 LD17114.5prime LD Drosophila melanogaster ... 38 1.1
AA392544, AA392544 LD11451.5prime LD Drosophila melanogaster ... 38 1.1
AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1
AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1
AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1
AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1
AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1
AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1
AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1
AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1
AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1
AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1
AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3
C19706, C19706 Rice cDNA, partial sequence (E10809_1A) 36 4.3
D41773, RICS4574A Rice cDNA, partial sequence (S4574_2A). 36 4.3
C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3
AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3
C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
D46016, RICS10393A Rice cDNA, partial sequence (S10393_3A). 36 4.3
AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3
AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3
D46541, RICS11289A Rice cDNA, partial sequence (S11289_1A). 36 4.3
D47315, RICS12612A Rice cDNA, partial sequence (S12612_1A). 36 4.3
AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3
AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3
D47243, RICS12505A Rice cDNA, partial sequence (S12505_1A). 36 4.3
AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A Rice cDNA, partial sequence (C0136A). 36 4.3
D46483, RICS11185A Rice cDNA, partial sequence (S11185_1A). 36 4.3
D46618, RICS11395A Rice cDNA, partial sequence (S11395_1A). 36 4.3
D46659, RICS11457A Rice cDNA, partial sequence (S11457_1A). 36 4.3
D46719, RICS11572A Rice cDNA, partial sequence (S11572_1A). 36 4.3
D48579, RICS14880A Rice cDNA, partial sequence (S14880_2A). 36 4.3
AA802334, AA802334 GM04219.5prime GM Drosophila melanogaster ... 36 4.3
D46066, RICS10470A Rice cDNA, partial sequence (S10470_1A). 36 4.3
D47037, RICS12104A Rice cDNA, partial sequence (S12104_1A). 36 4.3
D46874, RICS11807A Rice cDNA, partial sequence (S11807_2A). 36 4.3
D47174, RICS12340A Rice cDNA, partial sequence (S12340_2A). 36 4.3
T04578, T04578 625 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 36 4.3
C83675, C83675 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
D47950, RICS13762A Rice cDNA, partial sequence (S13762_1A). 36 4.3
R90044, R90044 16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 4.3
D46994, RICS12013A Rice cDNA, partial sequence (S12013_2A). 36 4.3
AA440820, AA440820 LD15713.5prime LD Drosophila melanogaster ... 36 4.3
C72089, C72089 Rice cDNA, partial sequence (E0963_1A) 36 4.3
Z84004, SSZ84004 S.scrofa mRNA; expressed sequence tag (5'; ... 36 4.3
D47519, RICS13070A Rice cDNA, partial sequence (S13070_1A). 36 4.3
C19735, C19735 Rice cDNA, partial sequence (E10858_1A) 36 4.3
D47231, RICS12462A Rice cDNA, partial sequence (S12462_1A). 36 4.3
D47147, RICS12293A Rice cDNA, partial sequence (S12293_1A). 36 4.3
AA950198, AA950198 LD30147.5prime LD Drosophila melanogaster ... 36 4.3
Z47624, ATTS4480 A. thaliana transcribed sequence; clone TAI... 36 4.3
D45955, RICS10259A Rice cDNA, partial sequence (S10259_1A). 36 4.3
D47137, RICS12280A Rice cDNA, partial sequence (S12280_1A). 36 4.3
D69927, CELK093H2F C.elegans cDNA clone yk93h2 : 5' end, sin... 36 4.3
AA392275, AA392275 LD11117.5prime LD Drosophila melanogaster ... 36 4.3

SEQ ID NO:546

D87455, D87455 Human mRNA for KIAA0266 gene, complete cds 1164 0.0
Z99129, HS425C14 Human DNA sequence from clone 425C14 on chr... 42 0.20
D90900, D90900 Synechocystis sp. PCC6803 complete genome, 2/... 40 0.80
Z74281, SCYDL233W S.cerevisiae chromosome IV reading frame O... 38 3.1
AL021528, HS394P21 Homo sapiens DNA sequence from PAC 394P21... 38 3.1
Z49155, HSL83D3 Human DNA from cosmid L83d3, Huntington's Di... 38 3.1
U33761, HSU33761 Human cyclin A/CDK2-associated p45 (Skp2) mR... 38 3.1
AF052832, AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 38 3.1
Z98600, SPAC20G4 S.pombe chromosome I cosmid c20G4 38 3.1

Y09438, SPHUSPLUS S.pombe hus1+ gene 38 3.1
D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0
AA824593, AA824593 oc83d10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 670 0.0
AA954862, AA954862 op20c03.s1 NCI_CGAP_Co12 Homo sapiens cDNA... 581 e-164
T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145
R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143
AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142
AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104
R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103
AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65
AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44
AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5
AA992442, AA992442 or85h03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79
AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035
W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035
AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035
AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2
AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2
AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2
AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2
AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2
AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2
AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9
C40718, C40718 C.elegans cDNA clone yk247f9 : 5' end, single... 36 1.9
AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9
AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.67
AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.67
AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67
AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67
AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67
AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67
W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67
AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67
AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67
AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.67
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.67
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67
AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67
N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67
AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.67
AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67
AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.67
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67
AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.67
AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.67
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.6
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7

AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.7
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.7
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.053
C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.84
AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.84
AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84
AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84
AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.84
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.84
AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.84
AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.3
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.3
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.3
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.3
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.3
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.3
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34
U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3
AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 3e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64
AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.64
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.64
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64
AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.64
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.64
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.5
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.81
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.2
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.2
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.2
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.2
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.2
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.2
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.2

SEQ ID NO:549

U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0
AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28
AC004636, AC004636 Homo sapiens chromosome 5, P1 clone 1268h6... 42 0.28
M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28
AC002097, AC002097 Homo sapiens chromosome 9q34, clone 246H5,... 42 0.28
AB006709, AB006709 Vibrio alginolyticus rpoN gene for RNA po... 42 0.28
Z47074, CEK07C10 Caenorhabditis elegans cosmid K07C10, compl... 40 1.1
AC004755, AC004755 Homo sapiens chromosome 19, fosmid 37502, ... 40 1.1
Z28051, SCYKL051W S.cerevisiae chromosome XI reading frame O... 40 1.1
AF022655, AF022655 Homo sapiens cep250 centrosome associated ... 40 1.1
AB006708, AB006708 Arabidopsis thaliana genomic DNA, chromos... 40 1.1
AF049105, AF049105 Homo sapiens centrosomal Nek2-associated p... 40 1.1
Z28050, SCYKL050C S.cerevisiae chromosome XI reading frame O... 40 1.1
X75781, SCXI286K S.cerevisiae chromosome XI (28.6 kb) DNA fo... 40 1.1
Y16899, DMY16899 Drosophila melanogaster mRNA for optomotor-... 38 4.3
M87854, RATBARK1 Rattus norvegicus beta-adrenergic receptor k... 38 4.3
M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3
M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3
D84549, YSACA Candida tropicalis DNA for carnitine acetyltra... 38 4.3
L23127, RATRMCI Rattus norvegicus germline MHC class I gene, ... 38 4.3
AC004257, AC004257 Homo sapiens chromosome 19, cosmid R33209,... 38 4.3
U70850, CELF28F9 Caenorhabditis elegans cosmid F28F9 38 4.3
U88309, CELT23B3 Caenorhabditis elegans cosmid T23B3 38 4.3
X53421, DVCHOS18 D. virilis s18, s15, s19, s16 chorion prote... 38 4.3
D89245, D89245 Schizosaccharomyces pombe mRNA, partial cds, ... 38 4.3
AF009623, AF009623 Parascaris univalens PUMA1 (puma1) mRNA, c... 38 4.3
S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3
Z67883, CEK02A4 Caenorhabditis elegans cosmid K02A4, complet... 38 4.3
U90567, GGU90567 Gallus gallus glutamine rich protein mRNA, p... 38 4.3
M98498, BOVEZRINA Bos taurus ezrin mRNA, complete cds. 38 4.3
M34073, MUSMHT10C Mus musculus (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3
X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3
U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3
U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0
AA886109, AA886109 ny44f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 656 0.0
AA829894, AA829894 oe51e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 650 0.0
AA879456, AA879456 oj91g03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 650 0.0
AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0
W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0
AI033069, AI033069 ow93f02.s1 Soares_fetal_liver_spleen_1NFLS... 642 0.0
AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0
N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180
N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180
H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180
AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180
R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178
AA744290, AA744290 ny51d02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA... 626 e-177
AI038590, AI038590 ox34e03.s1 Soares_total_fetus_Nb2HF8_9w Ho... 624 e-177
AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177
AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176
AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173
R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167
R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167
H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165
R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164
AA910762, AA910762 ol25h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 559 e-157
AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156
AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153
R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151
H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150
N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149
D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129
H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122
AA971254, AA971254 op73c08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 442 e-122
W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118
AA878973, AA878973 oj26d11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 389 e-106
AA715235, AA715235 nv10g01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96
AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74
AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69
AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41
T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40
N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38
AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18
AI038890, AI038890 ox84g12.x1 Soares_senescent_fibroblasts_Nb... 40 0.53
D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1
AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1
AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1
AA742364, AA742364 ny89c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
AA907234, AA907234 ol03h08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1
AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1
AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1
W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1
AI039908, AI039908 ox25f07.x1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
AA280664, AA280664 zs99f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
AA973566, AA973566 oo46f09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1
AA995707, AA995707 os29c09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
AI016407, AI016407 ot72e09.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1
AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA938631, AA938631 oo96f07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103
AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44
AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41
AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38
AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10
AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07
AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19
AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19
AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75
AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75
W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75
AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0
AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0
AA230895, AA230895 mw14g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0
W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0
AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0
W66734, W66734 me26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0
AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0
AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0
AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0
AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0
AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0
AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0
AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316... 36 3.0
W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0
AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0

AA784124, AA784124 d2b06a1.f1 Aspergillus nidulans 24hr asexu... 38 0.67
AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6
AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6
F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6
AA786697, AA786697 k5d01a1.f1 Aspergillus nidulans 24hr asexu... 36 2.6
AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 0.80
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 0.80
Y14330, HSY14330 Homo sapiens partial mRNA for jagged2 protein 38 3.2
AF003521, AF003521 Homo sapiens Jagged 2 mRNA, complete cds 38 3.2
AF029778, AF029778 Homo sapiens Jagged2 (JAG2) mRNA, complete... 38 3.2
AF020201, AF020201 Homo sapiens Jagged 2 mRNA, complete cds 38 3.2
Z71523, SCYNL247W S.cerevisiae chromosome XIV reading frame ... 38 3.2
AF029779, AF029779 Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2
U70049, RNU70049 Rattus norvegicus jagged2 precursor gene, pa... 38 3.2
X96722, SCCHXIVL S.cerevisiae DNA region from chromosome XIV... 38 3.2
AF005938, AF005938 Cavia porcellus L-type voltage-dependent c... 38 3.2
X78972, SBSTRBF S.bluensis ISP 5564 genes strB and strF 38 3.2
X94912, HSPR22 H.sapiens Pr22 gene 38 3.2

HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-144
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 2e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 2e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 1e-90
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 1e-84
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 1e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.098
AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.39
AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.39
AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.39
AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.39
AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39

AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39
AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.39
AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39
AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39
AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39
W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39
AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39
N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39
AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.39
AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39
AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 1.5
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.14
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.14
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.14
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.14
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.14
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031
AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48
AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48
AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48
AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48
AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48
AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48
AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 1.9
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.68
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.68
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.68
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.68
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.68
AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.68
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.68
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.68
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.7
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.7
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.7
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.7
R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.7

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
AA250010, AA250010 mz59b12.r1 Soares mouse lymph node NbMLN M... 38 0.97
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97
AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 3.8
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 3.8
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 3.8
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.8
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.8
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.8
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.8
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AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 3.8
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 3.8
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.8
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.8
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.8
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 3.8
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 3.8
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 3.8
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.8
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.8
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 3.8
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8
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AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.8
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 3.8
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 3.8
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.8
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 3.8
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.8

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055
AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22
Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22
AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22
H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22
AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22
Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.4
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.4
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4
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D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.4

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U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72
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AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.72
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72
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AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8
N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
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AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26
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AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26
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AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 4.0
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C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.0
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AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0
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AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 4.0
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AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0
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W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
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AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 4.0
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 4.0
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 4.0

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.058
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AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.90
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.6
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.6
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.6
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.6
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5
L02053, OMMGSHTR1 Ommastrephes sloani glutathione transferase... 38 3.5
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0
AA557183, AA557183 nl74f12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 874 0.0
AA761171, AA761171 nz09e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 866 0.0
AA976975, AA976975 oq26g11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 854 0.0
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0
AA909198, AA909198 ol12d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 831 0.0
W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0
W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0
W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0
AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0
H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0
W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0
AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0
AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0
AA662309, AA662309 nu97c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 668 0.0
W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176
N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165
AA251287, AA251287 zs04c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 583 e-164
AA971082, AA971082 op70h01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 567 e-160
W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159
AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157
AA729063, AA729063 nw22f08.s1 NCI_CGAP_GCB0 Homo sapiens cDNA... 557 e-157
AA987313, AA987313 or81h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 553 e-155
AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152
AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148
N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146
AA947355, AA947355 od86e12.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 504 e-140
AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127
AA742964, AA742964 ny15d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 454 e-126
AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125
W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123
W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121
AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109
N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106
N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104
AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99
AA936553, AA936553 on23g11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 361 9e-98
N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95
AA834628, AA834628 od98a10.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 341 8e-92
AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92
AA909616, AA909616 ol09d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 341 8e-92
H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86
AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84
AA911960, AA911960 oh88g08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 317 1e-84
AA969099, AA969099 op55e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 2e-80
AA766191, AA766191 oa12g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 5e-53
AA689312, AA689312 nx05e10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
AA534939, AA534939 nf82f03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 167 3e-39
AA888430, AA888430 nw74e05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 167 3e-39
N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34
AA535102, AA535102 nf84f06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 135 1e-29
AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28
AA766681, AA766681 oa34c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 105 9e-21
AA761492, AA761492 nz27a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 101 1e-19
AA688350, AA688350 nv15a05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 90 5e-16
AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12
T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'. 46 0.007
AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007
AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43
AA904415, AA904415 ok07e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.43
AI018800, AI018800 ov32h04.x1 Soares_testis_NHT Homo sapiens ... 38 1.7
AA631083, AA631083 nq77e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94
AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82
AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52
AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48
AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45
AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41
AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41
AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36
W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25
AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22
AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05
AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61
AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61
AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61
AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4
AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4
AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4
W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4
AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4
AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4
AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4
AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4
W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4
AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4
AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4
AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14
F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54
H91505, H91505 SWMFCA089SK Brugia malayi microfilaria cDNA (S... 36 2.1
AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1
AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1
AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0
Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048
U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19
AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19
AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19
U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75
L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75
M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75
L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75
J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75
M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75
X72711, MMREPCFC M.musculus mRNA for replication factor C, 1... 38 3.0
M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0
U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0
AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0
J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0
J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0
X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0
X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0
D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0
Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0
D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0
Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0
L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0
U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0
U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0
K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0
Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0
U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0
Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

HUMAN ESTs

SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0
S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005
Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019
AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073
X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.29
U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29
X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29
U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29
Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29
U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29
Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29
X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29
X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29
L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29
U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1
S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1
U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1
Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1
U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 1.1
X58857, SCPPH22 S.cerevisiae PPH22 gene for protein phosphat... 40 1.1
X79379, SCPROIS S.cerevisiae gene for proline isomerase 40 1.1
Z68341, CEF01G4 Caenorhabditis elegans cosmid F01G4, complet... 40 1.1
M17192, MUSHOX1 Mouse homeodomain protein (Hox1.1) mRNA, comp... 40 1.1
U50307, CELF43H9 Caenorhabditis elegans cosmid F43H9. 40 1.1
S73144, S73144 bone sialoprotein [cattle, fetal bone cells, m... 40 1.1
L34569, YSCFPR3A Saccharomyces cerevisiae (clone pBYNG1) prol... 40 1.1
D78303, D78303 Rattus norvegicus YT521 mRNA for RNA splicing... 40 1.1
X83276, SCDNAIV S.cerevisiae DNA for ORFs from chromosome IV 40 1.1
U54558, HSU54558 Human translation initiation factor eIF3 p66... 40 1.1
Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 1.1
X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 1.1
AB011125, AB011125 Homo sapiens mRNA for KIAA0553 protein, p... 40 1.1
Z46373, SC8248 S.cerevisiae chromosome XIII cosmid 8248 40 1.1
AF039042, CELZK697 Caenorhabditis elegans cosmid ZK697 40 1.1
Z28028, SCYKL028W S.cerevisiae chromosome XI reading frame O... 40 1.1
AC005266, AC005266 Homo sapiens chromosome 19, cosmid F23465,... 38 4.5
U60822, HSU60822 Human dystrophin (DMD) gene, exons 7, 8 and ... 38 4.5
AJ003141, HVAJ3141 Hordeum vulgare mRNA for stress-related p... 38 4.5
M26250, CRAGAP43 Goldfish (C.auratus) growth-associated prote... 38 4.5
X95267, GGRYR3 G.gallus mRNA for ryanodine receptor type 3 38 4.5
L37092, MUSCDPK Mus musculus cyclin-dependent kinase homologu... 38 4.5
Z72507, CEF17C11 Caenorhabditis elegans cosmid F17C11, compl... 38 4.5
U29608, DMU29608 Drosophila melanogaster large tumor suppress... 38 4.5
Z49072, CET24A11 Caenorhabditis elegans cosmid T24A11, compl... 38 4.5
M83142, RATBGASTR Rattus norvegicus beta-galactoside-alpha 2,... 38 4.5
Z20656, HSCAMHCA Homo sapiens of cardiac alpha-myosin heavy ... 38 4.5
M82937, YSACS2A Candida albicans chitin synthase 2 (CHS2) gen... 38 4.5
U28888, MMU28888 Mus musculus neurogenic differentiation fact... 38 4.5
S66408, S66408 c-erbB=proto-oncogene {exon 1, promoter} [chic... 38 4.5
AC002396, AC002396 Arabidopsis thaliana chromosome I BAC F3I6... 38 4.5
AE000665, MMAE000665 Mus musculus TCR beta locus from bases 5... 38 4.5
L39837, DROWARTS Drosophila melanogaster tumor supressor (war... 38 4.5
AG000377, AG000377 Homo sapiens genomic DNA, 21q region, clo... 38 4.5
X05632, HSMHCAG1 Human alpha-MHC gene for myosin heavy chain... 38 4.5
AC002108, AC002108 Genomic sequence from Mouse 4, complete se... 38 4.5
U37219, HSU37219 Human cyclophilin-like protein CyP-60 mRNA, ... 38 4.5
M58633, MUSP58GTA Mouse p58/GTA protein kinase mRNA, complete... 38 4.5
M25162, HUMMYHC08 Human cardiac alpha-myosin heavy chain (MYH... 38 4.5
Z46259, SCRPD3COS S.cerevisiae FY1676 RPD3 gene. 38 4.5
U09558, LJU09558 Lactobacillus johnsonii ATCC 11506 insertion... 38 4.5
U66160, MMUSC104 Mus musculus extracellular matrix associated... 38 4.5
Z73126, SCYLL021W S.cerevisiae chromosome XII reading frame ... 38 4.5
U83981, HSU83981 Homo sapiens apoptosis associated protein (G... 38 4.5

U59897, MRU59897 Macropus robustus hypoxanthine phosphoribosy... 38 4.5
D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5
X69838, HSG9A H.sapiens mRNA for G9a 38 4.5
X52952, RNCMOSO Rat mRNA for c-mos 38 4.5
U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5
X65880, DPRH4OP1 D.pseudoobscura rh4 opsin gene, exon 1 38 4.5
U58971, NTU58971 Nicotiana tabacum calmodulin-binding protein... 38 4.5
Z35773, SCYBL012C S.cerevisiae chromosome II reading frame O... 38 4.5
X67668, MMHMG2 M.musculus mRNA for high mobility group 2 pro... 38 4.5
L81727, HSL81727 Homo sapiens (subclone 1_d5 from P1 H69) DNA... 38 4.5
AL023800, HS833B2 Human DNA sequence *** SEQUENCING IN PROGR... 38 4.5
X62438, HVPERO H.vulgare mRNA for peroxidase 38 4.5
AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5
AL008980, PFSC03050 Plasmodium falciparum DNA *** SEQUENCING... 38 4.5
U64827, MMU64827 Mus musculus extracellular matrix associated... 38 4.5
AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 38 4.5
AE001002, AE001002 Archaeoglobus fulgidus section 105 of 172 ... 38 4.5
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 38 4.5
M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5
M77637, CHKEGF Gallus gallus EGF/TGF-alpha receptor (c-erbB) ... 38 4.5
U08185, MMU08185 Mus musculus BALB/c zinc-finger protein Blim... 38 4.5
AC004231, AC004231 Homo sapiens chromosome 17, clone hRPC.111... 38 4.5
Z50100, HVC39SAT H.vulgare GAA-satellite DNA 38 4.5
X53731, SCSPA2G S. cerevisiae SPA2 gene 38 4.5
U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5
X97560, SC32KBF S.cerevisiae 32kb DNA fragment of chromosome... 38 4.5
AB011479, AB011479 Arabidopsis thaliana genomic DNA, chromos... 38 4.5
U89340, LVU89340 Lytechinus variegtus Endo16 homolog (LvEndo1... 38 4.5
U73850, TCU73850 Trypanosoma cruzi 29 kDa proteasome subunit ... 38 4.5
AB006698, AB006698 Arabidopsis thaliana genomic DNA, chromos... 38 4.5
D37888, CYIMYC2 Cyprinus carpio c-myc gene for c-Myc, comple... 38 4.5
AF017349, MMDSGIII 7 Mus musculus desmoglein 3 (Dsg3) gene, i... 38 4.5
X91807, OSTA136 O.sativa mRNA for alpha-tubulin (clone OSTA-... 38 4.5
Z71587, SCYNL311C S.cerevisiae chromosome XIV reading frame ... 38 4.5
AE000742, AE000742 Aquifex aeolicus section 74 of 109 of the ... 38 4.5

HUMAN ESTs

AA324311, AA324311 EST27136 Cerebellum II Homo sapiens cDNA 5... 593 e-167
AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 513 e-143
AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141
AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 502 e-140
AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 502 e-140
AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 502 e-140
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 502 e-140
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 502 e-140
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 464 e-128
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84
R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68
AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14
AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14
AA928679, AA928679 on48e08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 40 0.55
AA887972, AA887972 nq95g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55
AA887862, AA887862 nq99b08.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
AA554819, AA554819 ni34d08.s1 NCI_CGAP_Lu1 Homo sapiens cDNA ... 40 0.55
AA557362, AA557362 nl81d12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55
N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55
AA552228, AA552228 nk06b04.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 40 0.55
AI017648, AI017648 ou99b02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA... 40 0.55
T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55
AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55
AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55
N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55
AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55
AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55
AA731625, AA731625 nw64a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55
R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55
AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55
AA633213, AA633213 nq57c06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.55
W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55
AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55
N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55
N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
AI041637, AI041637 ox92h08.x1 Soares_senescent_fibroblasts_Nb... 40 0.55
N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55

AA535094, AA535094 nf84e06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA514414, AA514414 nf57d11.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55
N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55
AA535811, AA535811 nf93g10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55
AA534433, AA534433 nf80a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55
AA970859, AA970859 oo81h03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.55
F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55
AA810279, AA810279 od14g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA595146, AA595146 nl84b01.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA632386, AA632386 np67e06.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55
AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55
AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55
AA961724, AA961724 or60a10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 40 0.55
AA551210, AA551210 nj27e09.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 40 0.55
R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55
AA938086, AA938086 oj08h08.s1 NCI_CGAP_Mel3 Homo sapiens cDNA... 40 0.55
AA576021, AA576021 nm57d11.s1 NCI_CGAP_Br3 Homo sapiens cDNA ... 40 0.55
AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55
AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55
W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55
AA632245, AA632245 np67b09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55
R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55
AI028447, AI028447 ow08b09.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.55
AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55
AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA815223, AA815223 oc05c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55
AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA643849, AA643849 np26f07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.55
AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55
AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA535972, AA535972 nf95a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA866044, AA866044 oh52g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.55
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 167 1e-39
AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.78
AA413261, AA413261 ve52f04.r1 Beddington mouse embryonic regi... 38 0.78
AA097645, AA097645 mm36f09.r1 Stratagene mouse skin (#937313)... 38 0.78
AA122578, AA122578 mn25b08.r1 Beddington mouse embryonic regi... 38 0.78
AA122581, AA122581 mn25c08.r1 Beddington mouse embryonic regi... 38 0.78
AA646168, AA646168 vn11e06.r1 Stratagene mouse Tcell 937311 M... 36 3.1
AA200881, AA200881 mu03c09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 3.1
AA217675, AA217675 mv01b09.r1 Soares mouse lymph node NbMLN M... 36 3.1
AI006387, AI006387 ua71d09.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 3.1
AA207387, AA207387 mv89a11.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 3.1
AA123112, AA123112 mn30g01.r1 Beddington mouse embryonic regi... 36 3.1
AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 3.1
AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 3.1
W12171, W12171 ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.1
AA208446, AA208446 mv85e01.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 3.1
AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 3.1
AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 3.1
AA561847, AA561847 vl27a12.r1 Stratagene mouse Tcell 937311 M... 36 3.1
AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 3.1
AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
AA052080, AA052080 mf69f12.r1 Soares mouse embryo NbME13.5 14... 36 3.1
AA000646, AA000646 mg23f09.r1 Soares mouse embryo NbME13.5 14... 36 3.1
AA510521, AA510521 vh59a05.r1 Soares mouse mammary gland NbMM... 36 3.1
AI006122, AI006122 ua86h01.r1 Soares mouse mammary gland NbMM... 36 3.1
AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 3.1
W77413, W77413 me64d06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
AA114809, AA114809 mn17e09.r1 Beddington mouse embryonic regi... 36 3.1
AA793564, AA793564 vn54c05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.1
AA174537, AA174537 mt10f09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
W62181, W62181 md87d08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.1
AA286005, AA286005 va30e05.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 3.1
AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 44 0.011
AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 44 0.011
AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 44 0.011
C70525, C70525 C.elegans cDNA clone yk409g6 : 5' end, single... 44 0.011
AA520235, AA520235 TgESTzz53c06.r1 TgME49 invivo Bradyzoite c... 42 0.044
T42800, T42800 6063 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 42 0.044
R29976, R29976 12581 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 42 0.044
H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.18
AA819924, AA819924 MF5MA171.AE3 S. mansoni female adult Lambd... 40 0.18
H37128, H37128 15257 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
T04367, T04367 414 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 40 0.18
R90528, R90528 16883 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
AA660422, AA660422 00298 MtRHE Medicago truncatula cDNA 5' 40 0.18
U94861, RRU94861 Rattus norvegicus clone HCY3 mRNA sequence 40 0.18
F14275, ATTS5197 A. thaliana transcribed sequence; clone YBY... 38 0.69
W43730, W43730 23107 CD4-16 Arabidopsis thaliana cDNA clone H... 38 0.69
N65025, N65025 20065 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 38 0.69
AI001628, AI001628 EST0210 Tilapia brain cDNA library in pUC1... 38 0.69
H74687, H74687 383 Brassica napus cDNA clone R25R. 38 0.69
AA395597, AA395597 27394 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.69
D41274, RICS3647A Rice cDNA, partial sequence (S3647_1A). 38 0.69
Z25731, ATTS1208 A. thaliana transcribed sequence; clone VCV... 38 0.69
N82780, N82780 TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 0.69
AA597822, AA597822 29889 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
AA948906, AA948906 LD27590.5prime LD Drosophila melanogaster ... 38 0.69
AI013695, AI013695 EST208370 Normalized rat spleen, Bento Soa... 38 0.69
AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.69
F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 2.7
T46158, T46158 9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
C91400, C91400 Dictyostelium discoideum slug cDNA, clone SSK169 36 2.7
T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AA440655, AA440655 LD15510.5prime LD Drosophila melanogaster ... 36 2.7
AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A Schistosom... 36 2.7
Z32623, ATTS2751 A. thaliana transcribed sequence; clone YAP... 36 2.7
T43683, T43683 6946 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AA263535, AA263535 LD06645.5prime LD Drosophila melanogaster ... 36 2.7
C37095, C37095 C.elegans cDNA clone yk482c11 : 3' end, singl... 36 2.7

C57017, C57017 C.elegans cDNA clone yk308h9 : 3' end, single... 36 2.7
C93857, C93857 Dictyostelium discoideum slug cDNA, clone SSL794 36 2.7
C92242, C92242 Dictyostelium discoideum slug cDNA, clone SSD283 36 2.7
Z33976, ATTS3037 A. thaliana transcribed sequence; clone YAP... 36 2.7
R62091, R62091 EST351 Strongylocentrotus purpuratus cDNA 5' end. 36 2.7
AA567455, AA567455 HL01288.5prime HL Drosophila melanogaster ... 36 2.7
C74456, C74456 Rice cDNA, partial sequence (E31357_1A) 36 2.7
AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7
C92456, C92456 Dictyostelium discoideum slug cDNA, clone SSE569 36 2.7
T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
R29905, R29905 12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 2.7
M79841, M79841 wEST00378 Caenorhabditis elegans cDNA clone CE... 36 2.7
Z17562, ATTS0136 A. thaliana transcribed sequence; clone TAT... 36 2.7
D71983, CELK084H2R C.elegans cDNA clone yk84h2 : 3' end, sin... 36 2.7
T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7
U83048, BTU83048 Bos taurus clone 0429 mRNA sequence 36 2.7
AA660182, AA660182 00022 MtRHE Medicago truncatula cDNA 5' si... 36 2.7
D48514, RICS14740A Rice cDNA, partial sequence (S14740_1A). 36 2.7
C90110, C90110 Dictyostelium discoideum slug cDNA, clone SSI103 36 2.7
H36880, H36880 15009 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 2.7
AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 2.7
C11922, C11922 C.elegans cDNA clone yk144a11 : 5' end, singl... 36 2.7
AA816691, AA816691 LD03795.5prime LD Drosophila melanogaster ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 M.musculus mRNA for exon from unknown gene 22A3 260 5e-67
Z83760, CICOS41 Ciona intestinalis DNA sequence from cosmid ... 40 0.94
Z75710, CED1081 Caenorhabditis elegans cosmid D1081, complet... 40 0.94
U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94
X99757, DMDYDTRO D.melanogaster mRNA for dystrophin 38 3.7
U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7
AC004118, AC004118 Drosophila melanogaster (P1 DS06238 (D26))... 38 3.7
U50313, CELF44C4 Caenorhabditis elegans cosmid F44C4. 38 3.7
AC004503, AC004503 Homo sapiens chromosome 5, P1 clone 1354A7... 38 3.7
M16840, WHTCPCA2 Wheat Asp-tRNA gene. 38 3.7
Y13381, RNAMPH1 Rattus norvegicus mRNA for amphiphysin, amph1 38 3.7
AC002994, AC002994 Homo sapiens chromosome 17, clone HRPC987K... 38 3.7
AB008271, AB008271 Arabidopsis thaliana genomic DNA, chromos... 38 3.7
D49701, ASNNIAD Aspergillus oryzae niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7
Z98555, PFSC03027 Plasmodium falciparum DNA *** SEQUENCING I... 38 3.7

HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0
U56653, HSU56653 Human heat shock inducible mRNA 769 0.0
AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0
AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0
AA314922, AA314922 EST186735 HCC cell line (matastasis to liv... 698 0.0
AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0
H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177
AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176
AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170
AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164
AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150
AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150
AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150
AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141
R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135
AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134
AA564849, AA564849 nj22c04.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 442 e-122
AA932576, AA932576 oo57g10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 440 e-121
AA876265, AA876265 oi12g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 434 e-120
AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118
U56654, HSU56654 Human heat shock inducible mRNA 426 e-117
AA746600, AA746600 nx18c02.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 406 e-111
AA876346, AA876346 oj24a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 406 e-111
W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110
AI034059, AI034059 ow14h11.x1 Soares_parathyroid_tumor_NbHPA ... 357 2e-96
AA662934, AA662934 nu92d09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 323 2e-86
AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80
AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78
R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73
T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65
AA731264, AA731264 nw57c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA768549, AA768549 oa67c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54
T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49
AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49
AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22
R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06
T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8
AA595230, AA595230 nl84g02.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0
AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167
AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151
W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128
AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69
AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53
AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43
AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32
AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23
AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23
AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15
AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13
AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65
AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6
AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6
AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21
AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15
C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11
C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06
AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57
AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57
AA660585, AA660585 00471 MtRHE Medicago truncatula cDNA 5' si... 38 0.57
L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57
AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57
C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3
C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3
C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3
AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3
AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3
AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3
C28238, C28238 Rice cDNA, partial sequence (C60429_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0
S51239, S51239 calreticulin [Aplysia californica=marine snail... 56 1e-05
Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.012
U25723, CPU25723 Cavia porcellus alpha-2B adrenoceptor gene, ... 44 0.047
AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19
U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.19
V01470, ZMZE01 Zea mays gene encoding a zein gene (clone lam... 42 0.19
U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19
X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.19
AE000926, AE000926 Methanobacterium thermoautotrophicum from ... 42 0.19
AC004135, AC004135 Genomic sequence for Arabidopsis thaliana ... 42 0.19
AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74
AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 0.74
AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74
X07699, MMNUCLEO Mouse nucleolin gene 40 0.74
X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74
M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74
M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74
U15972, MMU15972 Mus musculus homeobox (Hoxa7) gene, complete... 40 0.74
AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74
U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74
AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74
U26259, MMU26259 Mus musculus C2-H2 zinc finger protein mRNA,... 40 0.74
L48363, MUSZFPTR Mus musculus zinc finger protein gene, compl... 40 0.74
AC003113, AC003113 Arabidopsis thaliana BAC F24O1 chromosome ... 40 0.74
D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74
U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74
U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74
U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 0.74
Z48618, SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), ... 40 0.74
U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA, co... 40 0.74
Z72672, SCYGL150C S.cerevisiae chromosome VII reading frame ... 40 0.74
Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 0.74
AF013969, AF013969 Mus musculus antigen containing epitope to... 40 0.74
M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74
U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74
M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74
U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 0.74
U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74
L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene, ... 40 0.74
U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 0.74
U88539, MMU88539 Mus musculus chromatin structural protein ho... 40 0.74
U07704, HSU07704 Human protein kinase PITSLRE isoform PBETA21... 38 2.9
U07705, HSU07705 Human protein kinase PITSLRE isoform PBETA22... 38 2.9
AF019612, AF019612 Homo sapiens S2P mRNA, complete cds 38 2.9
U04818, HSU04818 Human protein kinase PITSLRE alpha 2-4 mRNA,... 38 2.9
AB002381, AB002381 Human mRNA for KIAA0383 gene, partial cds 38 2.9
AB009520, AB009520 Pyrococcus horikoshii OT3 genomic DNA, 13... 38 2.9
Z83848, HS57A13 Human DNA sequence from PAC 57A13 between ma... 38 2.9
AC004592, AC004592 Homo sapiens PAC clone DJ0244J05 from 5q31... 38 2.9
L11710, ZEFZCMYC Brachydanio rerio c-myc oncoprotein mRNA, co... 38 2.9
D43920, CHKMETASE Chicken mRNA for DNA (cytosine-5-)-methylt... 38 2.9
U49056, RNU49056 Rattus norvegicus CTD-binding SR-like protei... 38 2.9
U04824, HSU04824 Human protein kinase PITSLRE alpha 2-1 mRNA,... 38 2.9
U78045, HSU78045 Human collagenase and stromelysin genes, com... 38 2.9
U04816, HSU04816 Human protein kinase PITSLRE alpha 2-2 mRNA,... 38 2.9
U04817, HSU04817 Human protein kinase PITSLRE alpha 2-3 mRNA,... 38 2.9

HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 519 e-145
AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 450 e-124
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 402 e-110
AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 347 1e-93
AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93
AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 1e-93
AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 347 1e-93
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 299 2e-79
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 250 2e-64
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09
AA737681, AA737681 nw63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090
R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090
AA569993, AA569993 nm47h04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 42 0.090
R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090
R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090
AA812204, AA812204 ob84f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090

D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36
AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36
AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36
T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36
AA974278, AA974278 oq14d03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.36
W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36
H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36
AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36
N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36
H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36
AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36
W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36
T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36
AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4
AA993061, AA993061 ot92h08.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 1.4
R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4
H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4
W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4
N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4
AA630851, AA630851 nt57f04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 1.4
N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4
AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4
AA911761, AA911761 og19b01.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 38 1.4
AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4
AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4
AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4
F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4
AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4
AA908705, AA908705 ol01b09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.4
AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41
AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032
AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032
AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13
AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13
AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13
AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13
AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13
AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13
AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51
AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51
AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51
AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51
AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51
AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51
C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51
AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51
AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51
AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51
AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51
AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51
AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51
C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51
AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51
W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51
AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51
AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0
AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0
AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0
AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0
AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0
AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0
AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0
AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0
AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0
AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0
AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0
AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0
AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0
AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0
AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0
AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0
AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0
AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0
AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525 C.elegans cDNA clone yk409g6 : 5' end, single... 44 0.007
F15112, SSO4D09 S.scrofa mRNA; expressed sequence tag (5'; c... 42 0.029
AA684640, AA684640 EST104989 Rat PC-12 cells, untreated Rattu... 40 0.11
H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.11
AA660422, AA660422 00298 MtRHE Medicago truncatula cDNA 5' 40 0.11
C59696, C59696 C.elegans cDNA clone yk440e1 : 3' end, single... 38 0.45
AI008699, AI008699 EST203150 Normalized rat embryo, Bento Soa... 38 0.45
AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.45
T38461, T38461 EST103957 Saccharomyces cerevisiae cDNA 3' end. 38 0.45
C59257, C59257 C.elegans cDNA clone yk386b12 : 3' end, singl... 38 0.45
AA948906, AA948906 LD27590.5prime LD Drosophila melanogaster ... 38 0.45
AI001628, AI001628 EST0210 Tilapia brain cDNA library in pUC1... 38 0.45
H31962, H31962 EST106545 Rat PC-12 cells, untreated Rattus sp... 38 0.45
AA979509, AA979509 LD34118.5prime LD Drosophila melanogaster ... 38 0.45
D41274, RICS3647A Rice cDNA, partial sequence (S3647_1A). 38 0.45
C58362, C58362 C.elegans cDNA clone yk366a8 : 3' end, single... 38 0.45
C57756, C57756 C.elegans cDNA clone yk298b9 : 3' end, single... 38 0.45
AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.45
H74687, H74687 383 Brassica napus cDNA clone R25R. 38 0.45
C10513, C10513 C.elegans cDNA clone yk147e9 : 3' end, single... 38 0.45
C55569, C55569 C.elegans cDNA clone yk191d1 : 3' end, single... 38 0.45
C94819, C94819 Sus scrofa mRNA; expressed sequence tag (5'; ... 38 0.45
C32982, C32982 C.elegans cDNA clone yk338a12 : 3' end, singl... 38 0.45
AA816691, AA816691 LD03795.5prime LD Drosophila melanogaster ... 36 1.8
AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 36 1.8
AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 36 1.8
AA660182, AA660182 00022 MtRHE Medicago truncatula cDNA 5' si... 36 1.8
D71983, CELK084H2R C.elegans cDNA clone yk84h2 : 3' end, sin... 36 1.8
R29905, R29905 12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 1.8
AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 36 1.8
U83048, BTU83048 Bos taurus clone 0429 mRNA sequence 36 1.8
AA440655, AA440655 LD15510.5prime LD Drosophila melanogaster ... 36 1.8
AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A Schistosom... 36 1.8
C93857, C93857 Dictyostelium discoideum slug cDNA, clone SSL794 36 1.8
AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 36 1.8
T46158, T46158 9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 36 1.8
Z17562, ATTS0136 A. thaliana transcribed sequence; clone TAT... 36 1.8
AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 36 1.8
AA567455, AA567455 HL01288.5prime HL Drosophila melanogaster ... 36 1.8
AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 36 1.8
AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 36 1.8
AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 36 1.8
AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 36 1.8
C37095, C37095 C.elegans cDNA clone yk482c11 : 3' end, singl... 36 1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8
T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8
AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8
AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092
U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36
Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36
AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36
X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36
D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36
AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4
AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4
X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene 38 1.4
X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0
D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0
D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0
H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172
AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166
AA977877, AA977877 oq56d03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 571 e-161
AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159
AA972542, AA972542 oo82e01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 561 e-158
AA954270, AA954270 on72e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 557 e-157
AA740333, AA740333 ob23c02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 557 e-157
AA999722, AA999722 ov04c06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 555 e-156
AA970621, AA970621 op40h08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 551 e-155
AA932930, AA932930 oo04g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 541 e-152
AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152
W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152
AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152
R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150
AI027967, AI027967 ov84d04.x1 Soares_testis_NHT Homo sapiens ... 535 e-150
AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150
AI040961, AI040961 ov53d06.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
AI024835, AI024835 ov35h09.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
AA740667, AA740667 ob01g12.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 531 e-149
AA994527, AA994527 ou42h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 531 e-149
AA932728, AA932728 oo31g06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 529 e-149
AI001978, AI001978 ot39f03.s1 Soares_testis_NHT Homo sapiens ... 529 e-149
N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149
N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148
AA883578, AA883578 al46b08.s1 Soares NFL T GBC S1 Homo sapien... 527 e-148
AA890154, AA890154 al53f07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 525 e-147
AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147
AA456074, AA456074 aa17b07.s1 Soares NhHMPu S1 Homo sapiens c... 523 e-147
AA884285, AA884285 am32f04.s1 Soares NFL T GBC S1 Homo sapien... 523 e-147
AA969436, AA969436 op53e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA952918, AA952918 on55h11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA971938, AA971938 op88b01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146
AA865258, AA865258 og87d08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 519 e-146
AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146
AA972041, AA972041 op88e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 519 e-146
R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146
AA917965, AA917965 om37e04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA505880, AA505880 ni01a09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 517 e-145
AA906270, AA906270 oj98e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145
AA927156, AA927156 om20f05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 515 e-144
AA976254, AA976254 oo30f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 515 e-144
R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144
AA938552, AA938552 oo78g11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 513 e-144
AA483809, AA483809 ne41c08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 513 e-144
AA962659, AA962659 or31f10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 511 e-143
AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143
AA410432, AA410432 zv12c09.s1 Soares NhHMPu S1 Homo sapiens c... 511 e-143
AA775373, AA775373 ad19c07.s1 Soares NbHFB Homo sapiens cDNA ... 511 e-143
AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143
AA904368, AA904368 ol15d02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 509 e-143
AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142
R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141
AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141
H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141
N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141
AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 502 e-140
H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140
AA988977, AA988977 or87e11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 500 e-140
AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140
AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139
AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139
R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139
H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139
AA875917, AA875917 oj15a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 496 e-138
R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138
AA970616, AA970616 op40h03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 494 e-138
AA912408, AA912408 ol23a05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA910051, AA910051 ol40e08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137
R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136
AA954722, AA954722 oo84c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 488 e-136
R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136
R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136
AA885425, AA885425 am12h09.s1 Soares NFL T GBC S1 Homo sapien... 486 e-136
AA884231, AA884231 am32a01.s1 Soares NFL T GBC S1 Homo sapien... 484 e-135
AA885048, AA885048 am11a12.s1 Soares NFL T GBC S1 Homo sapien... 482 e-134
AA996162, AA996162 os14f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 482 e-134
AA748637, AA748637 ny10a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 482 e-134
AI031908, AI031908 ow47e12.x1 Soares_parathyroid_tumor_NbHPA ... 482 e-134
AA884703, AA884703 am18e02.s1 Soares NFL T GBC S1 Homo sapien... 480 e-134
AA928243, AA928243 on87c10.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
AI025986, AI025986 ow03a09.s1 Soares_parathyroid_tumor_NbHPA ... 478 e-133
AA897637, AA897637 oj72g07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 472 e-131
AA877346, AA877346 01c07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 472 e-131
AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131
AA832163, AA832163 oc91b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 470 e-131
R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131
N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128
R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126
AA579968, AA579968 ng51c03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 444 e-123
AA843427, AA843427 ak07g06.s1 Soares parathyroid tumor NbHPA ... 438 e-121
AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121
AA835882, AA835882 oc81d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 434 e-120
AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119
AA512970, AA512970 nj16b08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 432 e-119
R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118
AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114
H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111
AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110
AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103
AA577436, AA577436 nm96h06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 351 4e-95
AA516390, AA516390 nf55e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 6e-94
AA534533, AA534533 nf80h06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 341 3e-92
AA541583, AA541583 ni89f05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 311 3e-83
N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81
AA905015, AA905015 ok09b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 8e-81
AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76
AA939048, AA939048 op56h04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 256 2e-66
AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63
R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61
AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59
W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44
AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44
AA455577, AA455577 aa17b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42
AA583931, AA583931 nn64e04.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 172 2e-41
AA907332, AA907332 ol22g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 168 3e-40
R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37
W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36
AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30
AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19
H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19
AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18
AA931370, AA931370 oo03d01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 96 3e-18
AA501911, AA501911 ng54a08.s1 NCI_CGAP_Li2 Homo sapiens cDNA ... 94 1e-17
AA548419, AA548419 nj14g09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AA588892, AA588892 no23b06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AI025228, AI025228 ov40h08.x1 Soares_testis_NHT Homo sapiens ... 76 3e-12
R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11
R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06
N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04
H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04
H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011
N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70
AA614692, AA614692 np52b10.s1 NCI_CGAP_Br1.1 Homo sapiens cDN... 38 0.70
H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7
H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7
AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7
AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7
AA632009, AA632009 np74c07.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 2.7
H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7
AI022018, AI022018 ow64d01.x1 Soares_senescent_fibroblasts_Nb... 36 2.7
AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7
N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7
AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65
AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61
AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60
AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56
AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56
AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54
AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50
W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48
AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34
W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27
Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25
AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12
AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11
AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004
AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99
AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99
W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99
AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99
Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99
C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9
AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9
AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9
AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9
AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9
W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9
AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9
AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9
AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9
AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9
AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9
AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9
AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9
AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9
AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9
AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9
W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9
AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9
AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9

AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42
AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22
AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22
AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87
D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87
AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87
AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5
C20118, C20118 Rice cDNA, partial sequence (E11542_2A) 34 3.5
AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5
AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

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U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11
V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45
X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45
U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8
U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8
U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8
AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8
M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8
AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8
AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8
Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8
U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8
U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8
U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8
U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8
U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147
AA834501, AA834501 of21c02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 381 e-104
W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84
R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54
AA761660, AA761660 nz24b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 3e-53
AA887861, AA887861 nq99b07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 74 2e-11
AA644044, AA644044 nm20b12.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22
AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22
T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86
AA515882, AA515882 nf67f10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 38 0.86
AA664812, AA664812 nu69b05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA... 36 3.4
T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4
AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA916894, AA916894 og34g10.s1 NCI_CGAP_Br7 Homo sapiens cDNA ... 36 3.4
N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4
AA953544, AA953544 om79g06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 36 3.4
AA505576, AA505576 nh93f03.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 3.4
H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4
AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA595583, AA595583 nk92c04.s1 NCI_CGAP_Co11 Homo sapiens cDNA... 36 3.4
AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4
AA810167, AA810167 ob88a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 36 3.4
H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4
W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4
R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4
AA514234, AA514234 nf56e10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms
AA821640, AA821640 vw
AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001
T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069
AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1
AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1
AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1
AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3
R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3
AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

SEQ ID NO:560

X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 1082 0.0
N75131, N75131 yz29g07.r1 Soares multiple sclerosis 2NbHMSP H... 989 0.0
AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0
AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0
AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0
AA878521, AA878521 oj19c01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 844 0.0
AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0
W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0
AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0
N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0
N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0
AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0
AA768023, AA768023 oa60e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 728 0.0
AA872018, AA872018 oi05f08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 718 0.0
AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0
AA814881, AA814881 oa75e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 708 0.0
R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0
W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0
R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0
D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179
AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178
AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177
R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176
AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175
AA633335, AA633335 nq58h09.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 611 e-173
AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169
R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168
AA872617, AA872617 oi05g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 591 e-167
H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166
AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159
H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153
AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147
AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145
AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140
AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139
AA769090, AA769090 oa74e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 494 e-138
H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121
H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120
AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101
AA932620, AA932620 oo61h04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 365 4e-99
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66
R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66
AA229414, AA229414 nc47f12.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 246 3e-63
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52
AA249061, AA249061 114438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081
AA977111, AA977111 oq24c03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.32
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0
gb|AA510881|AA510881 vh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45
gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8
gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161
gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108
gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96
gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90
gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82
gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82
gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73
gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37
gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34
dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10
gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6
dbj|C22690|C22690 Rice cDNA, partial sequence (S5274_4A) 36 1.6
gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6
gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6
gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6
gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6
gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6
gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10
gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10
emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10
gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40
dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40
gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40
emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6
dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6
gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6
emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6
gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0
gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049
gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19
gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77
gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77
gb|T90524|T90524 yd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0
gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0
gb|AA586935|AA586935 nn68h03.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 38 3.0
gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0
gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0
gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0
gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0
gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0
gb|AA889618|AA889618 ak28f06.s1 Soares_testis_NHT Homo sapiens ... 38 3.0

gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1
gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1
gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1
gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1
gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1
gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1
dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1
gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1
gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1
gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3
gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3
gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3
gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3
gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3
gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3
dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3
gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3
gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3
gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK Brugia malayi infective larva cDNA... 40 0.24
gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated Rattus sp... 38 0.96
gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 Rattus nor... 38 0.96
gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 Rattus nor... 38 0.96
gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96
gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96
gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96
gb|R95272|R95272 SWOvL3CA167SK Onchocerca volvulus infective la... 36 3.8
gb|AA917208|AA917208 ka05f02.s1 Onchocerca volvulus infective l... 36 3.8
dbj|C62023|C62023 C.elegans cDNA clone yk249d5 : 5' end, single... 36 3.8
gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8
gb|AI043280|AI043280 TENU0920 T. cruzi epimastigote normalized ... 36 3.8
gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8
gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8
dbj|C62878|C62878 C.elegans cDNA clone yk296d4 : 5' end, single... 36 3.8
gb|AA915818|AA915818 SWOvL3CA1269SK Onchocerca volvulus infecti... 36 3.8
gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.8
gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8
gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.8
gb|H54977|H54977 HHU16a Sorghum bicolor cv. TX430 Sorghum bicol... 36 3.8

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gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082
gb|U50197|CELF25E2 Caenorhabditis elegans cosmid F25E2. 44 0.082
dbj|AB007727|AB007727 Arabidopsis thaliana genomic DNA, chromos... 44 0.082
gb|U02562|BSU02562 Bacillus subtilis N-acetylglucosaminidase (l... 42 0.32
dbj|D45048|BACORFX Bacillus subtilis gene for beta-N-acetylgluc... 42 0.32
emb|Z70683|CEF13B12 Caenorhabditis elegans cosmid F13B12, compl... 40 1.3
emb|AL023828|CEY17G7B Caenorhabditis elegans cosmid Y17G7B, com... 40 1.3
gb|U39740|CELZC64 Caenorhabditis elegans cosmid ZC64. 40 1.3
gb|AF006490|AF006490 Gossypium hirsutum adenine nucleotide tran... 40 1.3
emb|AL010170|PFSC03098 Plasmodium falciparum DNA *** SEQUENCING... 40 1.3
gb|U53701|GHU53701 Gossypium hirsutum alcohol dehydrogenase 2d ... 40 1.3

HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0
gb|AA251062|AA251062 zs07c10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0
gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165
gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154
gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148
gb|AA225705|AA225705 nc10b05.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 515 e-144
gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134
gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121
gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119
gb|AA250933|AA250933 zs07d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 426 e-117
gb|AA216370|AA216370 nc10b05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 398 e-109
gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108
gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108
gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97
gb|AA602297|AA602297 np25a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 281 1e-73
gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66
gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59
gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56
gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55
dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47
gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38
gb|AA642960|AA642960 60f07.s1 NCI_CGAP_Lym3 Homo sapiens cDNA... 147 4e-33
gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62
gb|AA521500|AA521500 aa73h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.62
gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62
gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4
dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4
gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104
gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93
gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60
gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60
gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44
gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05
gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001
gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001
gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004
gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056

gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88
gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88
dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88
gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88
gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88
gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5
gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5
gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5
emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5
gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5
gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5
gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5
gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78
gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78
gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78
gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78
gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1
dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1
gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1
gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.1
gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1
gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1
gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1
gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1
gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

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substantially identical to D86956

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gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41
gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23
gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23
gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23
gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22
emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21
gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19
gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17
gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15
gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14
gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13
gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13
emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13
emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12
gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12
gb|G29058|G29058 chicken STS ADL368 76 3e-11
gb|G29060|G29060 chicken STS ADL352 76 3e-11
gb|U34048|HDU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11
gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09
gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08
gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06
gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06
emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06
gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029
emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12
emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12
gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46
emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46
emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46
emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46
gb|L13767|STMSEC101A Streptomyus lividans sec101 gene, 5' end p... 42 0.46
emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8
gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8
dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8
gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8
gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8
emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8
gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8
emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8
gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0
gb|AA975279|AA975279 oq36e08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 900 0.0
gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0
gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0
gb|AA632259|AA632259 np67d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 730 0.0
gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0
gb|AA515175|AA515175 ng68f10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA... 615 e-174
gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172
gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165
gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165
gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163
gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163
gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157
gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149
gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147
gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139
gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134
gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129
gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125
gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115
gb|AA907095|AA907095 ol03b12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 414 e-113
gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67
gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55
gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55
gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52
gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47
gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24
N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109
gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105
gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93
gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82
gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62
gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57
gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57
dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57
gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17
gb|AA667535|AA667535 vv1°b12.r1 Stratagene mouse heart (#937316... 40 0.31
gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb|AA444814|AA444814 vg50e04.r1 Soares mouse mammary gland NbMM... 38 1.2
gb|AA763341|AA763341 vw53b12.r1 Soares mouse mammary gland NMLM... 38 1.2
gb|AA110827|AA110827 mp57a12.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
gb|AA691932|AA691932 vt06b04.r1 Barstead mouse myotubes MPLRB5 ... 38 1.2
gb|W77233|W77233 me61f11.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
gb|AA072872|AA072872 mm80g08.r1 Stratagene mouse embryonic carc... 38 1.2
gb|AA980630|AA980630 ua43f05.r1 Soares mouse mammary gland NbMM... 36 4.9
gb|AA065522|AA065522 ml54d09.r1 Stratagene mouse testis (#93730... 36 4.9
gb|AA982398|AA982398 uh07b08.r1 Soares mouse hypothalamus NMHy ... 36 4.9
gb|W62610|W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
gb|AA286651|AA286651 vb79b02.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.9
gb|AA399772|AA399772 vd70g05.r1 Beddington mouse embryonic regi... 36 4.9
gb|AA510475|AA510475 vg32h08.r1 Soares mouse mammary gland NbMM... 36 4.9
gb|AA109064|AA109064 ml63g02.r1 Stratagene mouse testis (#93730... 36 4.9
gb|AA033485|AA033485 mi42c08.r1 Soares mouse embryo NbME13.5 14... 36 4.9
gb|W57221|W57221 md59g10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
gb|AA467106|AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 36 4.9
gb|W97470|W97470 mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
gb|AA606917|AA606917 vm91c05.r1 Knowles Solter mouse blastocyst... 36 4.9
dbj|C78330|C78330 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
gb|AA013753|AA013753 mh26h12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
gb|AA145240|AA145240 mr12a03.r1 Soares mouse 3NbMS Mus musculus... 36 4.9
gb|AA245533|AA245533 mx03c11.r1 Soares mouse NML Mus musculus c... 36 4.9
gb|AA770893|AA770893 vt13a08.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
dbj|C79987|C79987 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
gb|AA014027|AA014027 mh24a12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
dbj|C89051|C89051 Mus musculus early blastocyst cDNA, clone 01B... 36 4.9
gb|AA058308|AA058308 mj59e09.r1 Soares mouse embryo NbME13.5 14... 36 4.9
gb|AA673826|AA673826 vu08h10.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
gb|AA637080|AA637080 vn07h04.r1 Knowles Solter mouse blastocyst... 36 4.9
gb|W44292|W44292 mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9

gb|AA955972|AA955972 UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor... 159 4e-37
gb|AA957275|AA957275 UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor... 157 2e-36
emb|Z84031|SSZ84031 S.scrofa mRNA; expressed sequence tag (5'; ... 111 9e-23
gb|AF041408|AF041408 Fragaria x ananassa clone FA110b 96 5e-18
gb|AA933116|AA933116 SWBmL3SA048T3 Brugia malayi L3 subtracted ... 58 1e-06
gb|AA933363|AA933363 SWBmL3SA615T3 Brugia malayi L3 subtracted ... 52 7e-05
gb|AA660164|AA660164 00001 MtRHE Medicago truncatula cDNA 5' si... 50 3e-04
gb|N37420|N37420 18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
gb|H35981|H35981 14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
gb|AA882627|AA882627 TENS0198 T. cruzi epimastigote normalized ... 44 0.018
gb|AI026481|AI026481 TENU0693 T. cruzi epimastigote normalized ... 42 0.070
gb|AA946369|AA946369 EST201868 Normalized rat lung, Bento Soare... 42 0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070
gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070
dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325_1A). 40 0.28
gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28
gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28
dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574_1A). 40 0.28
dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613_1A). 40 0.28
gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28
dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239_1A). 40 0.28
gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28
gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28
gb|AA660165|AA660165 00002 MtRHE Medicago truncatula cDNA 5' si... 40 0.28
emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28
dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302_1A). 40 0.28
gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28
gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28
gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28
dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634_1A). 40 0.28
dbj|C19261|C19261 Rice cDNA, partial sequence (E10176_1A) 40 0.28
dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588_1A). 40 0.28
dbj|C26556|C26556 Rice cDNA, partial sequence (C12586_1A) 40 0.28
dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548_1A). 40 0.28
dbj|C72152|C72152 Rice cDNA, partial sequence (E1094_3A) 40 0.28
dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305_2A). 40 0.28
gb|AI028926|AI0289 (and many others of similar score)

SEQ ID NO:565

emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2
gb|AE000660|HUAE000660 Homo sapiens T-cell receptor alpha delta... 40 1.2
emb|AL022333|HS474I12 Human DNA sequence *** SEQUENCING IN PROG... 38 4.6
emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6
gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6
gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6
gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6
gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6
gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6
gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6
gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6
gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6
emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6
emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6
gb|AC004753|AC004753 Homo sapiens chromosome 16, cosmid clone R... 38 4.6
gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

gb|M73323|TRFTRPREDA Crithidia fasciculata trypanothione reduct... 38 4.6

HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0
gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130
gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94_24 5' ... 133 5e-29
gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036
gb|AA661650|AA661650 nv02h12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA261982|AA261982 zs20d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA588219|AA588219 no24c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA250891|AA250891 zs06c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA244177|AA244177 nc05a02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 38 2.2
gb|AA715147|AA715147 nv10d05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA659887|AA659887 nv03a10.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA627890|AA627890 nq70a08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA603596|AA603596 np27b11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA613738|AA613738 np25h09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA715248|AA715248 nv10h06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AI038487|AI038487 ow25d12.x1 Soares_parathyroid_tumor_NbHPA ... 38 2.2
gb|AA252786|AA252786 zs26f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA287819|AA287819 zs50h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA564176|AA564176 nj04c08.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA643870|AA643870 np26h07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA280371|AA280371 zt05f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2
gb|AA587820|AA587820 nj06h05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA588443|AA588443 no22c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA568385|AA568385 nl88f06.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 38 2.2
gb|AA281831|AA281831 zt06c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2
gb|AA689530|AA689530 ns66e07.r1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA688300|AA688300 nv14a09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA687962|AA687962 nv13h04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA526586|AA526586 ni96f11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA642589|AA642589 nq73f04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA541594|AA541594 ni89g07.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA278713|AA278713 zs76h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2
gb|AA689473|AA689473 ns66e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA459023|AA459023 aa26a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07
gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2
gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2
gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2
gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2
gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2
gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2
gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8
gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8
gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 2.8
gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8
gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8
gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8
gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044_1A). 36 2.8
gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8
gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786_1A). 36 2.8
gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8
dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612_1A). 36 2.8
gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8
dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620_1A). 36 2.8
gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8
gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a fragment thereof,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules or a fragment thereof,

(d)

an antibody that binds to an expression product of NA group 1 nucleic acids,

(e)

an antibody that binds to an expression product of NA group 3 nucleic acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

(I)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5. A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

the protein,

(ii)

a peptide derived from the protein,

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,

as a determination of regression, progression or onset of said condition.

6. The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

7. The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

(c)

a cell which presents the complex of the peptide and MHC molecule of (iv).

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group 12 molecule.

13. The method of claim 5, wherein the nucleic acid molecule is a NA Group 13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group 14 molecule.

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group 15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

18. A pharmaceutical preparation for a human subject comprising

an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and

a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen.

20. The pharmaceutical preparation of claim 19, wherein the plurality is at least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected from the group consisting of

(1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof,

(2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof,

(3) a host cell expressing the isolated polypeptide, or functional variant thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

31. A composition comprising
an isolated agent that binds selectively a PP Group 1 polypeptide.

32. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 3 polypeptide.

33. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 11 polypeptide.

34. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 12 polypeptide.

35. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 13 polypeptide.

36. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 14 polypeptide.

37. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 15 polypeptide.

38. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 16 polypeptide.

39. The composition of claims 31-38, wherein the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides.

40. The composition of claims 31-38, wherein the agent is an antibody.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic agent.

43. The composition of matter of claim 42, wherein the conjugate is of the agent and a therapeutic or diagnostic that is a toxin.

44. A pharmaceutical composition comprising an isolated nucleic acid molecule selected from the group consisting of:

(1)
NA Group 1 molecules, and

(2)
NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule.

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different human cancer associated antigen.

47. The pharmaceutical composition of claims 44-46 further comprising an expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host cell recombinantly expressing the isolated nucleic acid molecule.

49. A pharmaceutical composition comprising an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier.

50. The pharmaceutical composition of claim 49, wherein the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

51. The pharmaceutical composition of claim 49, wherein the isolated polypeptide comprises at least two different polypeptides, each comprising a different human cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 12 polypeptides or HLA binding fragments thereof.

54. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. The pharmaceutical composition of claims 49-57, further comprising an adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 11 molecule or a fragment thereof.

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 13 molecule or a fragment thereof.

64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 15 molecule or a fragment thereof.

66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1 **(correct?)**,

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of contiguous nucleotides is selected from the group consisting of:

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising

a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

(a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising

administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I)

removing an immunoreactive cell containing sample from the subject,

(ii)

contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

(iii)

introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I)

identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

(ii)

transfecting a host cell with a nucleic acid selected from the group consisting of

(a) the nucleic acid molecule identified,

(b)

a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

(c)

deletions, substitutions or additions to (a) or (b), and

(d)

degenerates of (a), (b), or (c);

(iii)

culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

94. The method of claim 93, further comprising:

(a)

identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

(I) identifying cells from the subject which express abnormal amounts of the protein;

(ii) isolating a sample of the cells;

(iii) cultivating the cells, and

(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

```
HY-LU-12    KEESPPPPKYVHPLIGLLGEYGGDSDYEEEEEEEQTPPPQPRTAQPQKREEQTKKENEEDKLTDWNKLACLLCRRQFPNKEVL 970
LUCA15      PELVRNGDEENPLKRGLVAAYSGDSDNEE...................ELVERLESEEEKLADWKKMACLLCRRQFPNKDAL 662
DXS8237E    DLPKLASDDRPSPPRGLVAAYSGESDSEE...................EQERGGPEREEKLTDWQKLACLLCRRQFPSKEAL 233

HY-LU-12    TKHQQLSDLPKQHLETHRKIKQSEQELAYLERRERE.GKFKGRGNDRREKLQSFDSPERKRIKYSRETDS..DRKLVDKEDID 1050
LUCA15      VRHQQLSDLHKQNMDIYRRSRLSEQELEALELRERE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQPTKDGID 742
DXS8237E    TPHQQLSGLHKQHLKIHRRAHLSEHELEALEKNDMEQMKYRDRAAERREKYGIPEPPEPKRRKYGGISTASVDFEQPTKDGLC 316

HY-LU-12    TTSKGGCVQQATGWRKGTGLGYGHPGLASSEEAEGRMRGPSVGASGRTSKRQSNETYRDAVRRVMFARYKELD       1123
LUCA15      HSNIGNKMLQAMGWREGSGLGRKCQGITAPIEAQVRLKGAGLGAKGSAYGLSGADSYKDAVRKAMFARFIEME       815
DXS8237E    SDNIGSRMLQAMGWKEGSGLGRKKQGIVTPIEAQTRVRGSGLGARGSSYGVTSTESYKETLHKTMVTRFHEAQ       389
```

Figure 1

```
     AAGGAGGAGCGGGCCGTGGAGGCTTCGCCCCCTAGGTACTGCTATAACCAGAATTTGGTATAAAAAGGATTTACTTGTTGGGGCCCTCTTGATAAAAAGA  100
     GATGTGGGGGGATTCTCGACCTGCTAACAGAACTGGACCTTTTCGTGGCAGCCAAGAAGAAAGGTTTGCTCCCGGGTCGAACAGGATTATCCTCCTCCT  200
1     M  M  G  D  S  D  P  A  H  R  T  G  P  P  R  G  S  Q  F  E  R  F  A  P  G  N  H  R  D  Y  P  P  P
     CCCCTTAAGAGTCATGCTCAAGAGAGACACTCTGGCAACTTTCCTGGCAGAGATTCACTTCCCTTTGATTTCCAGGGGCATTCGGGGCCTCCTTTTGCAA  300
34    P  L  K  S  H  A  Q  E  R  H  S  G  N  F  P  G  R  D  S  L  P  F  D  F  Q  G  H  S  G  P  P  F  A
     ATGTAGAGGAGCATTCTTTCAGCTATGGAGCTAGAGACGGACCGCATGGGACTATCGAGGAGGGGAAGGACCTGGACATGATTTCAGGGGGGGAGATTT  400
67   N  V  E  E  H  S  F  S  Y  G  A  R  D  G  P  H  G  D  Y  R  G  G  K  G  P  G  H  D  F  R  G  G  D  F
     TTCGTCTTCTGATTTCCAGAGCAGAGATTCATCACAGTTGGACTTCAGGGGTAGGGACTCACATTCTCGGGATTTTCGGGATAGAGAAGGACCACCTATG  500
101    S  S  S  D  F  G  S  R  D  S  S  Q  L  D  F  R  G  R  D  T  H  S  G  D  F  R  D  R  E  G  P  P  M
     GACTATAGGGGTGGAGATGGTACTTCTATGGATTATAGAGGTAGGGAGGCACCTCATATGAACTACAGAGACAGGGATGCTCACGCTGTGGACTTCAGAG  600
134  D  Y  R  G  G  D  G  T  S  M  D  Y  R  G  R  E  A  P  H  M  N  Y  R  D  R  D  A  H  A  V  D  F  R
     GTAGGGATGCTCCTCCATCTGACTTCAGGGGCCGGGGCACTTATGATTTAGATTTTAGAGGCCGGGATGGATCCCATGCAGATTTTAGGGGCAGGGATTT  700
167  G  R  D  A  P  P  S  D  F  R  G  R  G  T  Y  D  L  D  F  R  G  R  D  G  S  H  A  D  F  R  G  R  E  L
     ATCAGATTTGGATTTTAGGGCCAGAGAACAGTCCCGTTCTGATTTTAGGAATAGAGATGTATCTGATTTGGACTTTAGAGACAAAGACGGAACACAAGTA  800
201    S  D  L  D  F  R  A  R  E  Q  S  R  S  D  F  R  N  R  D  V  S  D  L  D  F  R  D  K  D  G  T  Q  V
     GACTTTAGAGGCCGAGGTTCAGGTACTACTGATCTAGACTTTAGGGACAGGGATACGCCACATTCTGATTTCAGAGGTAGACACCGATCTAGGACTGATC  900
234  D  F  R  G  R  G  S  G  T  T  D  L  D  F  R  D  R  D  T  P  H  S  D  F  R  G  R  H  R  S  R  T  D
     AGGATTTTAGGGGCAGAGAGATGGGATCTTGTATGGAATTTAAAGATAGGGAGATGCCCCCCGTGGATCCAAATATTTTGGATTACATTCAGCCCTCTAC  1000
267  Q  D  F  R  G  R  E  M  G  S  C  M  E  F  K  D  R  E  M  P  P  V  D  P  N  I  L  D  Y  I  Q  P  S  T
     ACAAGATAGAGAACATTCTGGTATGAATGTGAACAGGAGAGAAGAATCCACACACGACCATACGATAGAAAGGCCTGCTTTTGGCATTCAGAAGGGAGAA  1100
301    Q  D  R  E  H  S  G  M  N  V  N  R  R  E  E  S  T  H  D  H  T  I  E  R  P  A  F  G  I  Q  K  G  E
     TTTGAGCATTCAGAAACAAGAGAAGGAGAAACACAAGGTGTAGCCTTTGAACATGAGTCTCCAGCAGACTTTCAGAACAGCCAAAGTCCAGTTCAAGACC  1200
334    F  E  H  S  E  T  R  E  G  E  T  Q  G  V  A  F  E  H  E  S  P  A  D  F  Q  N  S  Q  S  P  V  Q  D
     AAGATAAGTCACAGCTTTCTGGACGTGAAGAGCAGAGTTCAGATGCTGGTCTGTTTAAAGAAGAAGGCGGTCTGGACTTTCTTGGGCGGCAAGACACCGA  1300
367  Q  D  K  S  Q  L  S  G  R  E  E  Q  S  S  D  A  G  L  F  K  E  E  G  G  L  D  F  L  G  R  Q  D  T  D
     TTACAGAAGCATGGAGTACCGTGATGTGGATCATAGGCTGCCAGGAAGCCAGATGTTTGGCTATGGCCAGAGCAAGTCTTTTCCAGAGGGCAAAACTGCC  1400
401    Y  R  S  M  E  Y  R  D  V  D  H  R  L  P  G  S  Q  M  F  G  Y  G  Q  S  K  S  F  P  E  G  K  T  A
     CGAGATGCCCAACGGGACCTTCAGGATCAAGATTATAGGACGGGCCCAAGTGAGGAGAAACCCAGCAGGCTTATTCGATTAAGTGGGGTACCTGAAGATG  1500
434    R  D  A  Q  R  D  L  Q  D  Q  D  Y  R  T  G  P  S  E  E  K  P  S  R  L  I  R  L  S  G  V  P  E  D
```

Figure 2

1586

CCACAAAAGAAGAGATTCTTAATGCTTTTCGGACTCCTGATGGCAATCCTGTAAAGAACTTGCAGTTGAAGGAGTATAACACAGGTTACGACTATGGCTA 1600
467 A T K E E I L R A F R T P D G N P V K H L Q L K E Y N T G Y D Y G Y

1689

TGTCTGCGTCGAGTTTTCACTCTTGGAAGATGCCATCGGATGCCATGAAGCCCACCAGGGAACTCTAATGATCCAGGACAAAGAAGTTACCCTGGAGTAT 1700
501 V C V E F S L L E D A I G C H E A H Q G T L H I Q D K E V T L E Y

GTATCAAGCCTGGATTTTTGGTACTGCAAACGATGTAAGGCAAACATTGGTGGGCACCGATCTTCCTGTTCATTCTGCAAGAACCCAAGAGAAGTGACAG 1800
534 V S S L D F W Y C K R C K A N I G G H R S S C S F C K N P R E V T

AGGCCAAGCAAGAATTAATAACCTACCCTCAGCCTCAGAAAACATCCATACCAGCACCATTGGAAAAACAGCCCAACCAGCCCCTAAGACCAGCTGATAA 1900
567 E A K Q E L I T Y P Q P Q K T S I P A P S E K Q P N Q P L R P A D K

GGAACCTGAACCCAGGAAGAGGGAAGAAGGCCAAGAGTCACGCTTAGGACATCAAAAGAGACAAGCAGAAAGGTATCTGCCTCCTTCTCGAAGGGAAGGG 2000
601 E P E $\boxed{P\ R\ K\ R}$ E E G Q E S R L G H Q K R Q A E R Y L P P S R K E G

CCAACTTTCCGAAGAGACCGAGAGAGGCGAGTCATGGTCTGGAGAGACACGCCAGCATGGAGAGAGCAAAACTATCATGCTAAAGCGTATCTATCGTTCCA 2100
634 P T F R R D R E R E S D S G E T R Q D G E S K T I M L K R I Y R S

CACCACCTGAGGTGATAGTGGAAGTGCTGGAGCCCTATGTCCGCCTTACTACTGCCAACGTCCGTATCATCAAGAACAGAACAGGCCCTATGGGCATAC 2200
667 T P P E V I V E V L E P Y V R L T T A N V R I I K N R T G P M G H T

CTATGGCTTTATTGACCTCGACTCCCATGTGGAAGCTCTTCGTGTGGTGAAGATCTTACAGAACCTTGATCCGCCATTTAGCATTGATGGGAAGCATGTA 2300
701 Y G F I D L D S H V E A L R V V K I L Q N L D P P F S I D G K H V

GCTGTAAACCTGGCCACTGGAAAACGAAGAAATGATTCTGGCGACCATTCTGACCACATGCATTACTATCAGGGTAAAAAATATTTCCGAGATAGGAGG 2400
734 A V N L A T G K R R N D S G D H S D H M H Y Y Q G K K Y F R D R R

GAGGTGGCAGAAATTCAGACTGGTCTTCAGATACAAATCGACAAGGACAACAGTCATCATCTGACTGCTACATATATGATTCTGCTAGTGGCTACTATTA 2500
767 G G G R N S D W S S D T N R Q G Q Q S S S D C Y I Y D S A S G Y Y S

GTGACCCCTTGGCAGGAACTTATTATGACCCCAATACCCAGGGAGAAGTCTATGTGCCCCAGGATCCTGGATTACCTGAGGAAGAAGAGATCAAGGAAAAA 2600
801 D P L A G T Y Y D P N T Q G E V Y V P Q D P G L P E E E E I K E K

AAACCCACCAGTCAAGGAAAGTCAAGTAGCAAGAAGGAAAATTCTAAAAGAGATGGCAAGGAGAAAAAAGACAGAGGAGTGACGAGGTTTCAGGAAAAT 2700
834 K P T S Q G K S S S K K E N S K R D G K E K K D R G V T R F Q E N

CCAGTGAAGGCAAGGCCCCTGCAGAAGACGTCTTTAAGAAGCCTCTGCCTCCTACTGTGAAGAAGGAAGAGAGTCCCCCTCCACCTAAAGTGGTAAACCC 2800
867 A S E G K A P A E D V F K K P L P P T V K K E E S P P P P K V V N P

CCTGATCGGCCTCTTGGGTGAATATGGAGGAGACAGTGACTATGAGGAGGAAGAAGAGGAGGAACAGACCCCTCCCCCACAGCCCCGCACAGCACAGCCC 2900
901 L I G L L G E Y G G D S D Y E E E E E E E Q T P P P Q P R T A Q P

CAGAAGCGAGAGGAGCAAACCAAGAAGGAGAATGAAGAAGACAAACTCACTGACTGGAATAAACTGGCTTGTCTGCTTTGCAGAAGGCAGTTTCCCAATA 3000
934 Q K R E E Q T K K E N E E D K L T D W N K L A C L L C R R Q F P N

Fig 2 (cont'd)

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     AAGAAGTTCTGATCAAACACCAGCAGCTGTCAGACCTGCACAAGCAAAACCTGGAAATCCACCGGAAGATAAAACAGTCTGAGCAGGAGCTAGCCTATCT   3100
967  K  E  V  L  I  K  H  Q  Q  L  S  D  L  H  K  Q  N  L  E  I  H  R  K  I  K  Q  S  E  Q  E  L  A  Y  L

     GGAAAGGAGAGAACGAGAGGGAAAGTTTAAAGGAAGAGCAAATCATCCAGCGAAAAGCTCCAGTCTTTTGACTCTCCAGAAAGGAAACGGATTAAGTAC   3200
1001  E  K  R  E  R  E  G  K  F  E  G  E  S  R  D  R  R  E  K  L  Q  S  F  D  S  P  E  R  K  R  I  K  Y

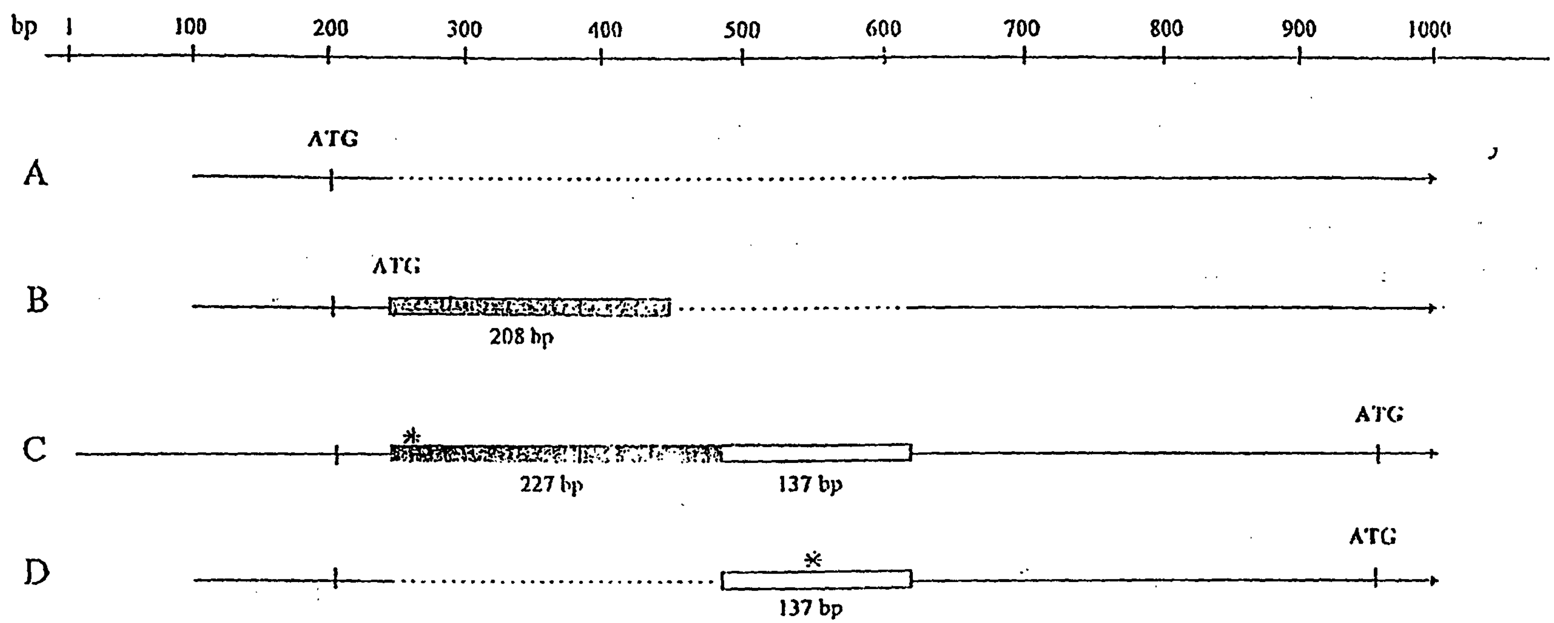
     TCTAGGGAAACTGACAGTGATCGTAAACTGGTTGATAAAGAAGATATCGACACTAGCAGCAAAGGAGGCTGTGTCCAACAGGCTACTGGCTGGAGGAAAG   3300
1034  S  R  E  T  D  S  D  R  K  L  V  D  K  E  D  I  D  T  S  S  K  G  G  C  V  Q  Q  A  T  G  W  R  K

     GGACAGGCCTGGGATATGGCCATCCTGGATTGGCTTCATCAGAGGAGGCTGAAGGCCGGATGAGGGGCCCCAGTGTTGGAGCCTCAGGAAGAACCAGCAA   3400
1067 G  T  G  L  G  Y  G  H  P  G  L  A  S  S  E  E  A  E  G  R  H  R  G  P  S  V  G  A  S  G  R  T  S  K

     AAGACAGTCCAACGAGACTTATCGAGATGCTGTTCGAAGAGTCCATGTTTGCTCGATATAAAGAACTCGATTAAGAAAGCAGACAAGTTCCATGGGATACA   3500
1101  R  Q  S  N  E  T  Y  R  D  A  V  R  R  V  H  F  A  R  Y  K  E  L  D ***

     ACCTCCCTCTTGTTTTGTTTGTCTCTCCTTTTCTTTTGTTACTGTTCTTGCTGCTAGAACTTTTTTAAATAAACTTTTTTTCAATGTGATTAAAAAAAA   3599
```

Fig 2(cont'd)



Transcript Variant B

```
AAGGAGGAGCGGGCCGTGGAGGCTTCGCCGCCTAGGTACTGCTATAACCAGAATTTGGTATAAAAAGGATTTACTTGTTGGGGCCCTCTTGATAAAAAGAGATGTGGGGGATTCTCGAC 120 (120)
CTGCTAACAGAACTGGACCTTTTCCAGATGGCGTTTCGCCGTGTTGGCCG[illegible]TCTCGGACTCCTGACCTCAAGTGATCCACCTACCTCGGCCTCCCAAAGTGCTGGGACTATAGGT 240 (145)
                   145  M  A  E  K  R  V  S  R  A  G  L  G  L  L  T  S  S  D  F  P  T  S  A  S  Q  S  A  G  T  I  G
GTGAGCCACCGCACCTGCCATTTGGATTGGCAATCTGCAA[illegible]TTTTATTA[illegible]TGCA[illegible]CAGATGTTCTCATTCATTGTTCTGAAGCTTGGAGTTCCAATGAAAAATTTAGTGGGAGC 360 (152)
 V  S  H  R  T  C  H  L  D  K  Q  S  A  R  F  Y  Y  L  H  A  T  D  V  L  I  H  C  S  E  A  W  S  S  H  E  K  F  S  G  S
CAAGAAGAAAGGTTTGCTCCCGGGTGG..
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Fig.3a

Figure 3b.

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137bp exon:
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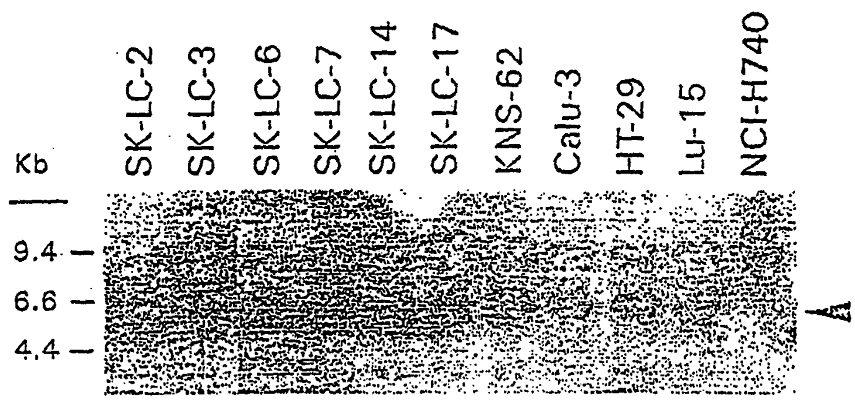
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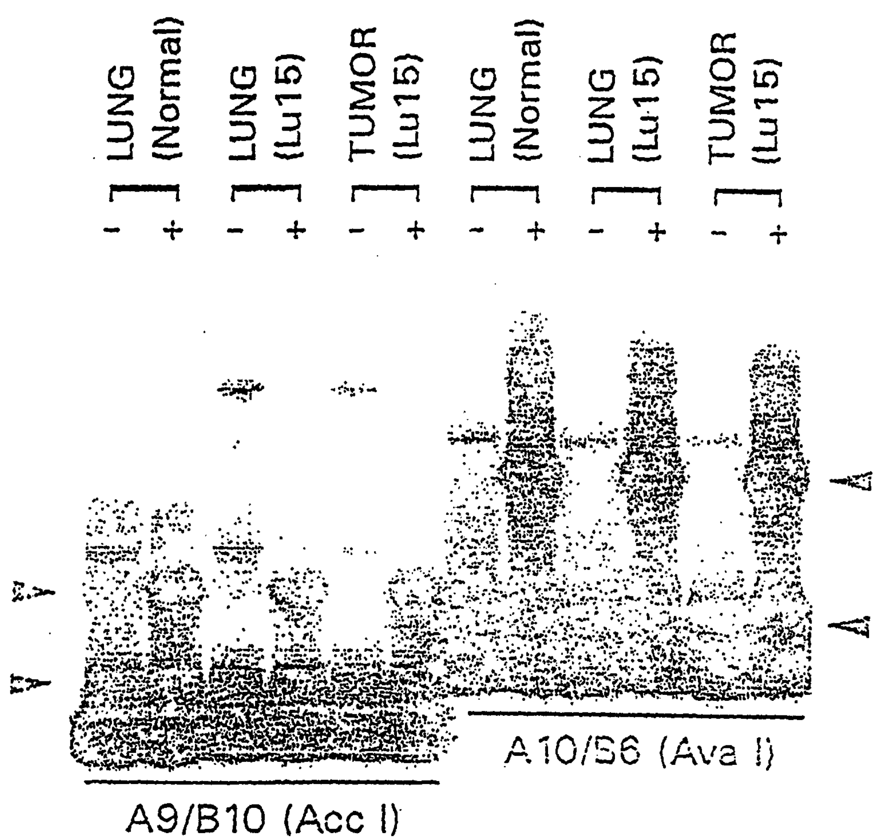
9.4
6.6
4.4

Figure 4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- + LUNG (Lu15)
- + TUMOR (Lu15)
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- + TUMOR (Lu15)
A9/B10 (Acc I)
A10/B6 (Ava I)

Figure 5

SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research
Old, Lloyd J.
Scanlan, Matthew J.
Stockert, Elisabeth
Gure, Ali
Chen, Yao-Tseng
Gout, Ivan
O'Hare, Michael
Obata, Yuichi
Pfreundschuh, Michael
Tureci, Ozlem
Sahin, Ugur

<120> CANCER-ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

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<150> U.S. 60/061,599
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<213> Homo Sapiens

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<212> DNA
<213> Homo Sapiens

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<212> DNA
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<211> 355
<212> DNA
<213> Homo Sapiens

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<212> DNA
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<211> 861
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<212> DNA
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<212> DNA
<213> Homo Sapiens

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<211> 374
<212> DNA
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<211> 552
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<211> 502
<212> DNA
<213> Homo Sapiens

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<211> 537
<212> DNA
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ccttttccag cactaccatt gtaaggtttt tttcaggagg gagggctaac caccttgctt   3000
ttctcttttc tctttttctt ttttttattt ttgttttatt aatttgggga aaggggtgtt   3060
agcattagtg ccatgatatc tactggattt taagtaggga gactttattt ttaaaggtag   3120
gttgaaattt gggagatttc tcggcaggaa gggctgaaat ccaggcccct gtctcaactt   3180
ggagagaggt gacagacggc agatcttcca aatcaaattc ctttccagtt cttcccctgg   3240
ctgccttttt gggggtccct gccttagccc cacacaaggc tttctgaact gccaagaggg   3300
gatctggctt ctcaactgct cggcctcttg ggccaggctg tgcccagcca gccctgggag   3360
aactgggtag caggtggctg acttctttaa gcacctttct aaataccagc agaagaggct   3420
cccgcctctg ttagcatgat cagtactatt gtgacattaa aacaacaaca ataagatctt   3480
cctatctgga gggtacagag gtgaatggct ttggttttca tttctctttc ttcactgctt   3540
ttctcggtgt ggtatttgac aagattttag ntnaaagcct caccatgaat tgattttttt   3600
tgtttgngng ngtgtttgtt ttgggacaat tttagatacc tgngtgcant ttttcagtta   3660
gtcctaantt ttaaaagaag ggnaaccaag nganatattt ggtgtaagtg ttgcagtatg   3720
aanttctggt tgcaatccct ccccgtccca cantgccccc catttgagta caccgcacaa   3780
gtcaaacgnt aggnagtttg nataaaacca atttttctaa nttgttgntc atttgttgta   3840
antcaataaa gcnaaganta aacattttta tt                                  3872
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<210> 31
<211> 655
<212> DNA
<213> Homo Sapiens

<400> 31

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gaaatcatgg gagcacaaag aagaaataag tgaagcagag ccaggggggtg gttccttggg     60
agatggaagg ccgccagagg aaagtgccca tgaaatgatg gaggaggaag aggaaatccc    120
aaaacctaag tctgtggttg caccgccagg tgctcctaag aaagagcatg taaatgtagt    180
attcattggg cacgtanatg ctggcaagtc aaccattgga ggacaaataa tgtatttgac    240
tggaatggtt gacaaaagga cgcttgaaaa gtatgaaaga gaagctaaag agaaaaacag    300
agaaacttgg tacttgtctt gggccttaga cacaaatcag gaagaacgag acaagggtaa    360
aacagtagaa gtgggtcgtg cctattttga aaccgaaaag aacatttcac aattctagat    420
atgaatccca gaacactgag ctcaaaaccc aaagcccaga atttgaagct caaagttccn    480
aattccanga aggtgcggag atgcttctga accccgagga aaagatcctt tgaatatctc    540
cgtaggagtt cacccccctgg actccttcac tcaggggttt ggggagcacc cacaggggac    600
ctgcccatag ggccaccttt tgagatgccc acaggggccc tgctgtctac accgc         655
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<210> 32
<211> 466
<212> DNA
<213> Homo Sapiens

<400> 32
gaaaggtggc cagaggaagg gacagctgac ctggcacaat ctgggcttga agggggcaca 60
acaagagcgt ctgtgagctg gtgctgtctg gagggatctt ggctcctctc cggctatctg 120
accttcctga agacctgctc gcacactgca tcccttgcag tcagttccag ctcgtgccga 180
attcggcacg agctcgtgcc gaattcggca cgagggaagc actactccca gcgctgggcc 240
caggaggacc tgctggagga gcagaaggat ggggcccggg cagcggctgt ggctgacaag 300
aagaaaggcc tcatggggcc actgaccgaa ctggacacta aagatgtgga tgccctgctg 360
aagaagtctg aggcccagca tgaacagccg gaagatggat gcccctttgg tgccctgacg 420
cagcgcctcc tgcaggccct ggtggaggaa aatattattt tttccc 466

<210> 33
<211> 293
<212> DNA
<213> Homo Sapiens

<400> 33
gtcggcgccc tacatgagaa gcatgatgca gtcgctgagc cagaatccag atttggctgc 60
acagatgatg ctgaatagcc cgctgtttac tgcaaatcct cagctgcagg agcagatgcg 120
gccacagctc ccagccttcc tgcagcagat gcagaatcca gacacactat cagccatgtc 180
aaacccaaga gcaatgcagg ctttaatgca gatccagcag ggctacaga cattagccac 240
tgaagcacct ggcctgattc cgagcttcac tccaggtgtg ggggtggggn tct 293

<210> 34
<211> 456
<212> DNA
<213> Homo Sapiens

<400> 34
caaagcctta agtcagagcc tgctagaatg tgtccaggtt tacagctata ctgcacagca 60
cttcccatgc tagtctctgt aaaacgcaaa aagccatttt caggagcagt aggcaagtca 120
cattcaattg aaatgcagga tggtgcactg ccattccaag ttccatcttc ctggcagatc 180
agcacagggt tccccagaag ttcatatcct ggattacagg tgtatgaaac catggtacca 240
tacagaaagt ttgatgaatg tgtagcagga gactcctttg tattttccca ggttttagcc 300
actgctccca aatgataagg agggtgagga gtcacatatg gaacttccat catgtcgtct 360
tcttgctcaa aatatccctg gtcatctttg agtttagtac agtctccaaa atctatatga 420
ggagggaggc cacagtctat tggcatacca aatttt 456

<210> 35
<211> 679
<212> DNA
<213> Homo Sapiens

<400> 35
ggcggcgttc gtgtccgagg tcactagttt cccggtagtt cagctgcaca tgaatagaac 60
agcaatgaga gccagtcaga aggactttga aaattcaata aatcaagtga aactcttgaa 120
aaaggatcca ggaaacgaag tgaagctaaa actctacgcg ctatataagc aggccactga 180
aggaccttgt aacatgccca aaccaggtgt atttgacttg atcaacaagg ccaaatggga 240
cgcatggaat gccccttggca gcctgcccaa ggaagctgcc aggcagaact atgtggattt 300
ggtgtccagt ttgagtcctt cattggaatc ctctagtcag gtggagcctg gaacagacag 360
gaaatcaact gggtttgaaa ctctggtggt gacctccgaa gatggcatca caaagatcat 420
gttcaaccgg cccaaaaaga aaaatgccat aaacactgag atgtatcatg aaattatgcg 480
tgcacttaaa gctgccagca aggatgactc aatcatcact gttttaacag gaaatggtga 540
ctattacagt agtgggaatg atctgactaa cttcactgat attccccctg gtggagtana 600
ggagaaagct aaaaataatg ccgttttact gaagggaatt tgtgggctgt tttatagaat 660
ttcctaagcc tctgattgc 679

<210> 36
<211> 689
<212> DNA
<213> Homo Sapiens

<400> 36
ctaaaccagt ggacatatca ggccatggtc cacgaactac taggcataaa caacaatcgg 60
attgatcttt ccagagtgcc gggaatcagt aaagacttaa gagaagtggt cctatctgct 120
gaaaatgatg aattctatgc taataatatg tacctgaact ttgctgagat tggtagcaat 180
ataaagaatc tcatggaaga ttttcagaag aagaaaccaa aagaacagca aaaactagaa 240
tcaatagcag acatgaaggc gtttgttgag aattatccac agttcaagaa aatgtctggg 300
actgtttcaa agcatgtgac agtggttgga gaactgtctc gattggtcag tgaacggaat 360
ctgctggagg tttcagaggt tgagcaagaa ctggcctgtc aaaatgacca ttctagtgct 420
ctccagaata taaaaaggct tctgcagaac cccaaagtga cagagtttga tgctgcccgc 480
ctggtgatgc tttatgcttt acattatgag cgacacagca gcaatagcct gccaggacta 540
atgatggncc tcaggaataa aggtgtttct gagaagtatc gaaagctcgt gtctgcagtt 600
gttgaatatg gtggtaaaac gagtcagagg aagtgacctc ctcagcccca aagatgctgt 660
tggctatcac caaacaattc ctcaaaggg 689

<210> 37
<211> 443
<212> DNA
<213> Homo Sapiens

<400> 37
ccacgcccgg ccccggagca ggcttttacg catgccccgc gcgccccctt gtgtccggaa 60
tttattcctt ccggtgggtt cgcggtctag ctgaccaaga acggaactgg ggactttcgc 120
agtgagagtt acagctctta aagatggcac cgacccaggc cgggcgcggt ggctcaggcc 180
tgcaatccca gcactttggg aggcggaggc aggtgaatca cgaggtcagg aaatcgagac 240
catcctggct aacatggtga aaccccgtct ccactaaaaa tacaaaaaat tagccaggca 300
tggtggctgg cacctgtagt cccagctact tgggaggctg agccaggaaa gtggcatgaa 360
cccgcgaggc agagcttgca ataagccgag atcgtgccaa tgcactccag cctgggcaac 420
agaaggagac actgtctcaa aaa 443

<210> 38
<211> 442
<212> DNA
<213> Homo Sapiens

<400> 38
ctcgcctcgg agcagccatg atggaaggcc tggacgacgg cccggacttc ctctcagaag 60
aggaccgcgg acttaaagca ataaatgtag atcttcaaag tgatgctgct ctgcaggtgg 120
acatttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagattc 180
caccagcacc accaagacct gattttgatg cttcaaggga aaaactacag aagcttggtg 240
aaggagaagg gtcaatgacg aaggaagaat tcacaaagat gaaacaggaa ctggaagctg 300
aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgtcgtgtgg 360
cagcacatcc tattttgaga agagatttaa atttccatgt cttcttggaa tataatcaag 420
atttgagtgt gcgaggaaaa aa 442

<210> 39
<211> 692
<212> DNA
<213> Homo Sapiens

<400> 39

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cagggacagg ccctatctta tatttttttc catcttcatc atccacttct gcttacagtt      60
tgctgcttac aataacttaa tgatggattg agttatctgg gtggtctcta gccatctggg     120
cagtgtggtt ctgtctaacc aaagggcatt ggcctcaaac cctgcatttg gtttaggggc     180
taacagagct cctcagataa tcttcacaca catgtaactg ctggagatct tattctatta     240
tgaataagaa acgagaagtt tttccaaagt gttagtcagg atctgaaggc tgtcattcag     300
ataacccagc ttttcctttt ggcttttagc ccattcagac tttgccagag tcaagccaag     360
gattgctttt ttgctacagt tttctgccaa atggcctagt tcctgagtac ctggaaacca     420
gagagaaaga ggatccagga tgtacttgga tgaggaggcc tggcttatct aggaagtcgt     480
gtctggggtg cttattgctg ctccatacag ctgtacgtca gccccttggc cttctctgta     540
ggttcttggc ancaatgagc agctttcact caagtgacac aagtaattac tgagtcctaa     600
tttgatagcc accaactgta cctgggtang caaagtcaga tttttgagaa nctttttcct     660
gatttgaagt tttaattacc ttaatttcct tt                                   692
```

<210> 40
<211> 619
<212> DNA
<213> Homo Sapiens

<400> 40

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gaggcaccag attctgctga ggggaccacc cttacagtgc tgcctgaagg tgaggagttg      60
cccctgtgtg tgagtgagag caatggcctg gagctcccac cctcagcagc atctgatgag     120
ccacttcagg agccactgga ggctgacagg acctcggaag agctgacaga ggccaagacc     180
ccaacctcca gcccagagaa gccacaggaa ctcgttacag ctgaggttgc agctccatcc     240
acctcatctt cagccacttc ctcgcctgag ggtccttcac ctgcccgacc tcctcggcgt     300
cgcaccagtg ctgatgtgga aattaggggt caagggactg gtcggccagg acaaccacca     360
ggccccaaag tgcttcgaaa gctgccagga cggctggtaa ctgtggtaga ggaaaaggaa     420
ctggtgcggc ggcggcggca gcagcgggga gctgccaanc accctagtgc ctggggtctc     480
tgagactagt gccagcccgg gaagcccgtc tgtccgcagc atgtcanggc canaatcctc     540
ccctcccatt ggtgggccct gtgaaagctg ctccttcatc cncactgcnc actccanccc     600
agnagccctt cattgcncg                                                  619
```

<210> 41
<211> 153
<212> PRT
<213> Homo Sapiens

<400> 41

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Pro Glu Ser Lys Pro Ile Met Thr Ser Ser Glu Ala Phe Glu Pro Pro
 1               5                  10                  15
Lys Tyr Leu Met Leu Gly Gln Gln Ala Val Gly Gly Val Pro Ile Gln
            20                  25                  30
Pro Ser Val Arg Thr Gln Met Trp Leu Thr Glu Gln Leu Arg Thr Asn
        35                  40                  45
Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
    50                  55                  60
Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
65                  70                  75                  80
Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
                85                  90                  95
Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
            100                 105                 110
Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
        115                 120                 125
Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
    130                 135                 140
```

Asp Ser Tyr Val Ala Ser Leu His His
145 150

<210> 42
<211> 95
<212> PRT
<213> Homo Sapiens

<400> 42
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val
1 5 10 15
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu
20 25 30
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu
35 40 45
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro
50 55 60
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Leu Lys Arg Met
65 70 75 80
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys
85 90 95

<210> 43
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 43
Ser Lys Leu Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr
1 5 10 15
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala
20 25 30
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro
35 40 45
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu
50 55 60
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly
65 70 75 80
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala
85 90 95
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu
100 105 110
Glu Gly

<210> 44
<211> 132
<212> PRT
<213> Homo Sapiens

<400> 44
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys
1 5 10 15
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys
35 40 45
Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro
50 55 60
Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His
65 70 75 80
Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg
85 90 95
Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly
100 105 110
His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu
115 120 125
Arg Glu Arg Ser
130

<210> 45
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 45
Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
1 5 10 15
Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
20 25 30
Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
35 40 45
Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
50 55 60
Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser
65 70 75 80
Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly
85 90 95
Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val
100 105 110
Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met
115 120 125
Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser
130 135 140
Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp
145 150 155 160
Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser
165 170 175
Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala
180 185 190
Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser
195 200 205
Arg Leu Ala Thr Arg Ser
210

<210> 46
<211> 248
<212> PRT
<213> Homo Sapiens

<400> 46

```
Gly Ser Arg Glu Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu
1               5                   10                  15
Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser
            20                  25                  30
Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser
        35                  40                  45
Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu
    50                  55                  60
His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala
65                  70                  75                  80
Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly
                85                  90                  95
Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn
            100                 105                 110
Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys
        115                 120                 125
Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser
    130                 135                 140
Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp
145                 150                 155                 160
Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met
                165                 170                 175
Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu
            180                 185                 190
Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg
        195                 200                 205
Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp
    210                 215                 220
Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp
225                 230                 235                 240
Glu Phe Ile His Lys Ile Thr Leu
                245
```

<210> 47
<211> 177
<212> PRT
<213> Homo Sapiens

<400> 47

```
Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu
1               5                   10                  15
Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile
            20                  25                  30
Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val
        35                  40                  45
Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr
    50                  55                  60
Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys
65                  70                  75                  80
Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser
                85                  90                  95
Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His
            100                 105                 110
Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly
```

```
        115                 120                 125
Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile
    130                 135                 140
Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys
145                 150                 155                 160
Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys
                165                 170                 175
Leu
```

<210> 48
<211> 102
<212> PRT
<213> Homo Sapiens

<400> 48

```
Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala
 1               5                  10                  15
Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly
            20                  25                  30
Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser
        35                  40                  45
Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro
    50                  55                  60
Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr
65                  70                  75                  80
Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu
                85                  90                  95
Pro Pro Leu Lys Asn Gly
            100
```

<210> 49
<211> 179
<212> PRT
<213> Homo Sapiens

<400> 49

```
His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly
 1               5                  10                  15
Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg
            20                  25                  30
Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr
        35                  40                  45
Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala
    50                  55                  60
Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val
65                  70                  75                  80
Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val
                85                  90                  95
Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu
            100                 105                 110
His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser
        115                 120                 125
Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu
    130                 135                 140
```

Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu
145 150 155 160
Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile
165 170 175
Cys Leu Leu

<210> 50
<211> 163
<212> PRT
<213> Homo Sapiens

<400> 50
Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys
1 5 10 15
Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu
20 25 30
Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile
35 40 45
Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly
50 55 60
His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly
65 70 75 80
Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln
85 90 95
Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln
100 105 110
Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala
115 120 125
Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg
130 135 140
Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu
145 150 155 160
Thr Leu Gln

<210> 51
<211> 164
<212> PRT
<213> Homo Sapiens

<400> 51
Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys
1 5 10 15
Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu
20 25 30
Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe
35 40 45
Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala
50 55 60
Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu
65 70 75 80
Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu
85 90 95
Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

```
            100                 105                 110
Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro
        115                 120                 125
Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg
    130                 135                 140
Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His
145                 150                 155                 160
Ile Ala Ile Ser


      <210> 52
      <211> 600
      <212> PRT
      <213> Homo Sapiens

      <400> 52
Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr
 1               5                  10                  15
Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser
            20                  25                  30
Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln
        35                  40                  45
Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser
    50                  55                  60
Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro
65                  70                  75                  80
Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr
                85                  90                  95
Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro
            100                 105                 110
Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr
        115                 120                 125
Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr
    130                 135                 140
Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser
145                 150                 155                 160
Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys
                165                 170                 175
Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly
            180                 185                 190
Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly
        195                 200                 205
Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val
    210                 215                 220
Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu
225                 230                 235                 240
Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile
                245                 250                 255
Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp
            260                 265                 270
Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe
        275                 280                 285
Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val
    290                 295                 300
Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro
```

305 310 315 320
Pro Thr Ile Thr Val Leu Pro Ala Gln Leu Ala Pro Thr Lys Met Thr
325 330 335
Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys Gln Ile Leu Gly Gln Thr
340 345 350
Ser Leu Val Leu Thr Gln Val Thr Ser Gly Ser Thr Thr Val Ser Cys
355 360 365
Ser Pro Ile Thr Leu Ala Val Ala Gly Val Thr Asn His Gly Gln Lys
370 375 380
Arg Pro Leu Val Thr Pro Gln Ala Ala Pro Glu Pro Lys Arg Pro His
385 390 395 400
Ile Ala Gln Val Pro Glu Pro Pro Pro Lys Val Ala Asn Pro Pro Leu
405 410 415
Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys Glu Gln Ile Ala His Leu
420 425 430
Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro Asp Asp Ala Glu Val Tyr
435 440 445
Arg Leu Ile Glu Val Thr Gly Leu Ala Arg Ser Glu Ile Lys Lys Trp
450 455 460
Phe Ser Asp His Arg Tyr Arg Cys Gln Arg Gly Ile Val His Ile Thr
465 470 475 480
Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala Ile Ala Ala Ser Arg His
485 490 495
Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe Ala Pro Gln Lys Phe Lys
500 505 510
Glu Lys Thr Gln Gly Gln Val Lys Ile Leu Glu Asp Ser Phe Leu Lys
515 520 525
Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp Arg Leu Arg Val Glu Thr
530 535 540
Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp Phe Ser Glu Arg Arg Lys
545 550 555 560
Leu Arg Asp Ser Met Glu Gln Ala Val Leu Asp Ser Met Gly Ser Gly
565 570 575
Gln Lys Arg Pro Arg Cys Gly Lys Pro Pro Met Val Leu Cys Leu Asp
580 585 590
Ser Asn Ser Ser Pro Val Pro Ser
595 600

<210> 53
<211> 163
<212> PRT
<213> Homo Sapiens

<400> 53
Arg Lys Ser Trp Glu His Lys Glu Glu Ile Ser Glu Ala Glu Pro Gly
1 5 10 15
Gly Gly Ser Leu Gly Asp Gly Arg Pro Pro Glu Glu Ser Ala His Glu
20 25 30
Met Met Glu Glu Glu Glu Glu Ile Pro Lys Pro Lys Ser Val Val Ala
35 40 45
Pro Pro Gly Ala Pro Lys Lys Glu His Val Asn His Val Ala Gly Lys
50 55 60
Ser Thr Ile Gly Gly Gln Ile Met Tyr Leu Thr Gly Met Val Asp Lys
65 70 75 80
Arg Thr Leu Glu Lys Tyr Glu Arg Glu Ala Lys Glu Lys Asn Arg Glu

```
                85                  90                  95
Thr Trp Tyr Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp
            100                 105                 110
Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Lys
        115                 120                 125
Lys His Phe Thr Ile Leu Asp Met Asn Pro Arg Thr Leu Ser Ser Lys
    130                 135                 140
Pro Lys Ala Gln Asn Leu Lys Leu Lys Val Pro Asn Ser Lys Val Arg
145                 150                 155                 160
Arg Cys Phe


      <210> 54
      <211> 155
      <212> PRT
      <213> Homo Sapiens

      <400> 54
Glu Arg Trp Pro Glu Glu Gly Thr Ala Asp Leu Ala Gln Ser Gly Leu
 1              5                   10                  15
Glu Gly Gly Thr Thr Arg Ala Ser Val Ser Trp Cys Cys Leu Glu Gly
            20                  25                  30
Ser Trp Leu Leu Ser Gly Tyr Leu Thr Phe Leu Lys Thr Cys Ser His
        35                  40                  45
Thr Ala Ser Leu Ala Val Ser Ser Ser Ser Cys Arg Ile Arg His Glu
    50                  55                  60
Leu Val Pro Asn Ser Ala Arg Gly Lys His Tyr Ser Gln Arg Trp Ala
65                  70                  75                  80
Gln Glu Asp Leu Leu Glu Glu Gln Lys Asp Gly Ala Arg Ala Ala Ala
                85                  90                  95
Val Ala Asp Lys Lys Lys Gly Leu Met Gly Pro Leu Thr Glu Leu Asp
            100                 105                 110
Thr Lys Asp Val Asp Ala Leu Leu Lys Lys Ser Glu Ala Gln His Glu
        115                 120                 125
Gln Pro Glu Asp Gly Cys Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu
    130                 135                 140
Gln Ala Leu Val Glu Glu Asn Ile Ile Phe Ser
145                 150                 155

      <210> 55
      <211> 112
      <212> PRT
      <213> Homo Sapiens

      <400> 55
Ser Glu Arg Ala Leu Ala Pro Arg Thr Tyr Arg Met Glu Thr Ala Arg
 1              5                   10                  15
Ser Ala Pro Tyr Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro
            20                  25                  30
Asp Leu Ala Ala Gln Met Met Leu Asn Ser Pro Leu Phe Thr Ala Asn
        35                  40                  45
Pro Gln Leu Gln Glu Gln Met Arg Pro Gln Leu Pro Ala Phe Leu Gln
    50                  55                  60
Gln Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala
65                  70                  75                  80
```

Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr
85 90 95
Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly
100 105 110

<210> 56
<211> 151
<212> PRT
<213> Homo Sapiens

<400> 56
Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe
1 5 10 15
Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu
20 25 30
Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His
35 40 45
Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala
50 55 60
Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys
65 70 75 80
Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu
85 90 95
Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys
100 105 110
Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr
115 120 125
Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu
130 135 140
Ala Gly Ser Asp Leu Arg Leu
145 150

<210> 57
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 57
Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His
1 5 10 15
Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
20 25 30
Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
35 40 45
Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
50 55 60
Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
65 70 75 80
Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
85 90 95
Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
100 105 110
Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
115 120 125
Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

130 135 140
Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
145 150 155 160
Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
165 170 175
Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
180 185 190
Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu
195 200 205
Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser
210 215 220

<210> 58
<211> 101
<212> PRT
<213> Homo Sapiens

<400> 58
Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
1 5 10 15
Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
20 25 30
Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser
35 40 45
Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
50 55 60
Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
65 70 75 80
Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
85 90 95
Thr Arg Asn Leu Cys
100

<210> 59
<211> 43
<212> PRT
<213> Homo Sapiens

<400> 59
Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
1 5 10 15
Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
20 25 30
Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
35 40

<210> 60
<211> 210
<212> PRT
<213> Homo Sapiens

<400> 60
Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
1 5 10 15
Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

```
            20                      25                      30
Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn
        35                      40                      45
Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu
    50                      55                      60
Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu
65                      70                      75                      80
Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys
                85                      90                      95
Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu
            100                     105                     110
Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu
        115                     120                     125
Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile
    130                     135                     140
Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg
145                     150                     155                     160
Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser
                165                     170                     175
Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr
            180                     185                     190
Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln
        195                     200                     205
Arg Lys
    210

      <210> 61
      <211> 40
      <212> PRT
      <213> Homo Sapiens

      <400> 61
Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu
 1               5                  10                  15
Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln
            20                  25                  30
Glu Arg Asn Trp Gly Leu Ser Gln
        35                  40

      <210> 62
      <211> 238
      <212> PRT
      <213> Homo Sapiens

      <400> 62
His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp
 1               5                  10                  15
Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln
            20                  25                  30
Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys
        35                  40                  45
Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val
    50                  55                  60
Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg
65                  70                  75                  80
```

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys
85 90 95
Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile
100 105 110
Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu
115 120 125
Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu
130 135 140
Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr
145 150 155 160
Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu
165 170 175
Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr
180 185 190
Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu
195 200 205
Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln
210 215 220
Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu
225 230 235

<210> 63
<211> 146
<212> PRT
<213> Homo Sapiens

<400> 63
Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe
1 5 10 15
Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln
20 25 30
Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg
35 40 45
Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro
50 55 60
Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu
65 70 75 80
Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu
85 90 95
Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
100 105 110
Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
115 120 125
Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
130 135 140
Gly Lys
145

<210> 64
<211> 63
<212> PRT
<213> Homo Sapiens

<400> 64
Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe

1 5 10 15
Ser Pro Asn Pro Arg Ile Val Ser Val Asn Ala Ser Tyr Ser Leu Ser
20 25 30
Asn Glu Ser Ser Leu Glu Gln Val Tyr Thr Leu Lys Met Ser Phe Ile
35 40 45
Ala Ser Asn Thr Tyr His Asn Gln Leu Tyr Lys Glu Gly Phe Leu
50 55 60

<210> 65
<211> 199
<212> PRT
<213> Homo Sapiens

<400> 65
Glu Ala Pro Asp Ser Ala Glu Gly Thr Thr Leu Thr Val Leu Pro Glu
1 5 10 15
Gly Glu Glu Leu Pro Leu Cys Val Ser Glu Ser Asn Gly Leu Glu Leu
20 25 30
Pro Pro Ser Ala Ala Ser Asp Glu Pro Leu Gln Glu Pro Leu Glu Ala
35 40 45
Asp Arg Thr Ser Glu Glu Leu Thr Glu Ala Lys Thr Pro Thr Ser Ser
50 55 60
Pro Glu Lys Pro Gln Glu Leu Val Thr Ala Glu Val Ala Ala Pro Ser
65 70 75 80
Thr Ser Ser Ser Ala Thr Ser Ser Pro Glu Gly Pro Ser Pro Ala Arg
85 90 95
Pro Pro Arg Arg Arg Thr Ser Ala Asp Val Glu Ile Arg Gly Gln Gly
100 105 110
Thr Gly Arg Pro Gly Gln Pro Pro Gly Pro Lys Val Leu Arg Lys Leu
115 120 125
Pro Gly Arg Leu Val Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg
130 135 140
Arg Arg Gln Gln Arg Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser
145 150 155 160
Glu Thr Ser Ala Ser Pro Gly Ser Pro Ser Val Arg Ser Met Ser Gly
165 170 175
Pro Glu Ser Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala Ala Pro Ser
180 185 190
Ser Ser Leu Pro Thr Pro Pro
195

<210> 66
<211> 1599
<212> DNA
<213> Homo Sapiens

<400> 66
ttctttgaaa cattattatt cagaacgaag gagaatgata cagatacact ggctgaggtg 60
ttttgaggtg cattgaaatg ttccatgctg ttacttaggt taacatgttc ttgaggtacc 120
atgccatgga ttaaaaggaa atttggtaag tggcttccac ctaaacgact tactagggaa 180
gctatgcgaa attatttaaa agggtaaggg gatcaaatag tacttatcct tcatgcaaaa 240
gttgtacaga agtcatatgg caatcaaaaa attttttttt gccctccccc ttgtgtatat 300
cttatgggca gtggatggaa gaaaaaaaaa gaacaaatga aatgcgatgg ttgttctgaa 360
cacagctctc atccatgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtacatatc tgattcagac 480

aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacggtga tgacattggt 540
gtgttcctca gcaagtagat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgtctcagga acaaaggtgg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa 780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat tttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
agagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat 1080
aaggcagggt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcactccaaa tttacgagtg tggtttgggg gggtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt 1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tggtccgaaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccgcg gccacattgc 1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta actaccgtct ttttgctag 1599

<210> 67
<211> 729
<212> PRT
<213> Homo Sapiens

<400> 67

Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
1 5 10 15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
20 25 30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
35 40 45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
50 55 60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65 70 75 80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
85 90 95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
100 105 110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
115 120 125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
130 135 140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145 150 155 160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
165 170 175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
180 185 190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
195 200 205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
210 215 220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

```
225                 230                 235                 240
His Val Lys Val Leu Asn Thr Ser Leu Lys Glu Lys Phe Asn Gly Lys
                245                 250                 255
Lys Ile Ile Ile Ile Ser Asp Tyr Leu Glu Tyr Asp Ser Leu Leu Glu
            260                 265                 270
Val Asn Glu Glu Ser Thr Val Ser Glu Ala Gly Pro Asn Gln Thr Phe
        275                 280                 285
Glu Val Pro Asn Lys Ile Ile Asn Arg Ala Lys Glu Thr Leu Lys Ile
    290                 295                 300
Asp Ile Leu His Lys Gln Ala Ser Gly Asn Ile Val Tyr Gly Val Phe
305                 310                 315                 320
Met Leu His Lys Lys Thr Val Asn Gln Lys Thr Thr Ile Tyr Glu Ile
                325                 330                 335
Gln Asp Asp Arg Gly Lys Met Asp Val Val Gly Thr Gly Gln Cys His
            340                 345                 350
Asn Ile Pro Cys Glu Glu Gly Asp Lys Leu Gln Leu Phe Cys Phe Arg
        355                 360                 365
Leu Arg Lys Lys Asn Gln Met Ser Lys Leu Ile Ser Glu Met His Ser
    370                 375                 380
Phe Ile Gln Ile Lys Lys Lys Thr Asn Pro Arg Asn Asn Asp Pro Lys
385                 390                 395                 400
Ser Met Lys Leu Pro Gln Glu Gln Arg Gln Leu Pro Tyr Pro Ser Glu
                405                 410                 415
Ala Ser Thr Thr Phe Pro Glu Ser His Leu Arg Thr Pro Gln Met Pro
            420                 425                 430
Pro Thr Thr Pro Ser Ser Ser Phe Phe Thr Lys Lys Ser Glu Asp Thr
        435                 440                 445
Ile Ser Lys Met Asn Asp Phe Met Arg Met Gln Ile Leu Lys Glu Gly
    450                 455                 460
Ser His Phe Pro Gly Pro Phe Met Thr Ser Ile Gly Pro Ala Glu Ser
465                 470                 475                 480
His Pro His Thr Pro Gln Met Pro Pro Ser Thr Pro Ser Ser Ser Phe
                485                 490                 495
Leu Thr Thr Leu Lys Pro Arg Leu Lys Thr Glu Pro Glu Glu Val Ser
            500                 505                 510
Ile Glu Asp Ser Ala Gln Ser Asp Leu Lys Glu Val Met Val Leu Asn
        515                 520                 525
Ala Thr Glu Ser Phe Val Tyr Glu Pro Lys Glu Gln Lys Lys Met Phe
    530                 535                 540
His Ala Thr Val Ala Thr Glu Asn Glu Val Phe Arg Val Lys Val Phe
545                 550                 555                 560
Asn Ile Asp Leu Lys Glu Lys Phe Thr Pro Lys Lys Ile Ile Ala Ile
                565                 570                 575
Ala Asn Tyr Val Cys Arg Asn Gly Phe Leu Glu Val Tyr Pro Phe Thr
            580                 585                 590
Leu Val Ala Asp Val Asn Ala Asp Ala Asn Met Glu Ile Pro Lys Gly
        595                 600                 605
Leu Ile Arg Ser Ala Ser Val Thr Pro Lys Ile Asn Gln Leu Cys Ser
    610                 615                 620
Gln Thr Lys Gly Ser Phe Val Asn Gly Val Phe Glu Val His Lys Lys
625                 630                 635                 640
Asn Val Arg Gly Glu Phe Thr Tyr Tyr Glu Ile Gln Asp Asn Thr Gly
                645                 650                 655
Lys Met Glu Val Val Val His Gly Arg Leu Asn Thr Ile Asn Cys Glu
            660                 665                 670
```

```
Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
        675                 680                 685
Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
    690                 695                 700
Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
705                 710                 715                 720
Met Glu Thr Ser Pro Asp Phe Phe Phe
                725
```

<210> 68
<211> 754
<212> PRT
<213> Homo Sapiens

<400> 68

```
Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro
 1               5                  10                  15
Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu
            20                  25                  30
Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe
        35                  40                  45
Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro
    50                  55                  60
Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys
65                  70                  75                  80
Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln
                85                  90                  95
Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr
            100                 105                 110
Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln
        115                 120                 125
Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile
    130                 135                 140
Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly
145                 150                 155                 160
Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His
                165                 170                 175
Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn
            180                 185                 190
Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His
        195                 200                 205
Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln
    210                 215                 220
Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr
225                 230                 235                 240
Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro
                245                 250                 255
Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu
            260                 265                 270
Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln
        275                 280                 285
Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys
    290                 295                 300
His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala
305                 310                 315                 320
```

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu
325 330 335
His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val
340 345 350
Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala
355 360 365
Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro
370 375 380
Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu
385 390 395 400
Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu
405 410 415
Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu
420 425 430
Ser Ser Ser Glu Glu Ser Ser Ser Glu Ser Ser Ser Glu Glu Glu Glu
435 440 445
Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Ser Glu Ser Ser Asp
450 455 460
Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu
465 470 475 480
Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser
485 490 495
Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys
500 505 510
Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly
515 520 525
Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser
530 535 540
Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro
545 550 555 560
Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala
565 570 575
Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser
580 585 590
Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn
595 600 605
Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala
610 615 620
Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp
625 630 635 640
Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val
645 650 655
Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys
660 665 670
Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu
675 680 685
Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys
690 695 700
Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln
705 710 715 720
Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser
725 730 735
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp
740 745 750
Ser Gly

<210> 69
<211> 210
<212> PRT
<213> Homo Sapiens

<400> 69
Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr
1 5 10 15
Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu
20 25 30
Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro
35 40 45
Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His
50 55 60
Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro
65 70 75 80
Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu
85 90 95
Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro
100 105 110
Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu
115 120 125
Gln Phe Leu Gln Gln Glu Leu Leu Ile Asn Ile Thr Glu His Glu Leu
130 135 140
Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu
145 150 155 160
Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly
165 170 175
Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys
180 185 190
Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu
195 200 205
Val Gln
210

<210> 70
<211> 621
<212> PRT
<213> Homo Sapiens

<400> 70
Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr
1 5 10 15
His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly
20 25 30
Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr
35 40 45
Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu
50 55 60
Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp
65 70 75 80
Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly
85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys
100 105 110
Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu
115 120 125
Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala
130 135 140
Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val
145 150 155 160
Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp
165 170 175
Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp
180 185 190
Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe
195 200 205
Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp
210 215 220
Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys
225 230 235 240
Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala
245 250 255
Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn
260 265 270
Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys
275 280 285
Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys
290 295 300
Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val
305 310 315 320
Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu
325 330 335
Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu
340 345 350
Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp
355 360 365
Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys
370 375 380
Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala
385 390 395 400
Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu
405 410 415
Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg
420 425 430
Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly
435 440 445
Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys
450 455 460
Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile
465 470 475 480
Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala
485 490 495
Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His
500 505 510
Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu
515 520 525
His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

```
    530                 535                 540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys
545                 550                 555                 560
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg
                565                 570                 575
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys
            580                 585                 590
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala
        595                 600                 605
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys
    610                 615                 620
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<210> 71
<211> 267
<212> PRT
<213> Homo Sapiens

<400> 71

```
Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp
 1               5                  10                  15
Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn
            20                  25                  30
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro
        35                  40                  45
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu
    50                  55                  60
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp
65                  70                  75                  80
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe
                85                  90                  95
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn
            100                 105                 110
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu
        115                 120                 125
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys
    130                 135                 140
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile
145                 150                 155                 160
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala
                165                 170                 175
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile
            180                 185                 190
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys
        195                 200                 205
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu
    210                 215                 220
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln
225                 230                 235                 240
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys
                245                 250                 255
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr
            260                 265
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<210> 72
<211> 1752

<212> PRT
<213> Homo Sapiens

<400> 72
Arg Glu Lys Arg Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
1 5 10 15
Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
20 25 30
Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
35 40 45
Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
50 55 60
Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
65 70 75 80
Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
85 90 95
Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
100 105 110
Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
115 120 125
Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
130 135 140
Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
145 150 155 160
Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
165 170 175
Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
180 185 190
Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
195 200 205
Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
210 215 220
Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
225 230 235 240
Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
245 250 255
Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
260 265 270
Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
275 280 285
Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
290 295 300
Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
305 310 315 320
Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
325 330 335
Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
340 345 350
Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
355 360 365
Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
370 375 380
Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
385 390 395 400
Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

405 410 415
Thr Arg Leu Arg Ile Asp Tyr Glu Arg Val Ser Gln Glu Arg Thr Val
420 425 430
Lys Asp Gln Asp Ile Thr Arg Phe Gln Asn Ser Leu Lys Glu Leu Gln
435 440 445
Leu Gln Lys Gln Lys Val Glu Glu Glu Leu Asn Arg Leu Lys Arg Thr
450 455 460
Ala Ser Glu Asp Ser Cys Lys Arg Lys Lys Leu Glu Glu Glu Leu Glu
465 470 475 480
Gly Met Arg Arg Ser Leu Lys Glu Gln Ala Ile Lys Ile Thr Asn Leu
485 490 495
Thr Gln Gln Leu Glu Gln Ala Ser Ile Val Lys Lys Arg Ser Glu Asp
500 505 510
Asp Leu Arg Gln Gln Arg Asp Val Leu Asp Gly His Leu Arg Glu Lys
515 520 525
Gln Arg Thr Gln Glu Glu Leu Arg Arg Leu Ser Ser Glu Val Glu Ala
530 535 540
Leu Arg Arg Gln Leu Leu Gln Glu Gln Glu Ser Val Lys Gln Ala His
545 550 555 560
Leu Arg Asn Glu His Phe Gln Lys Ala Ile Glu Asp Lys Ser Arg Ser
565 570 575
Leu Asn Glu Ser Lys Ile Glu Ile Glu Arg Leu Gln Ser Leu Thr Glu
580 585 590
Asn Leu Thr Lys Glu His Leu Met Leu Glu Glu Glu Leu Arg Asn Leu
595 600 605
Arg Leu Glu Tyr Asp Asp Leu Arg Arg Gly Arg Ser Glu Ala Asp Ser
610 615 620
Asp Lys Asn Ala Thr Ile Leu Glu Leu Arg Ser Gln Leu Gln Ile Ser
625 630 635 640
Asn Asn Arg Thr Leu Glu Leu Gln Gly Leu Ile Asn Asp Leu Gln Arg
645 650 655
Glu Arg Glu Asn Leu Arg Gln Glu Ile Glu Lys Phe Gln Lys Gln Ala
660 665 670
Leu Glu Ala Ser Asn Arg Ile Gln Glu Ser Lys Asn Gln Cys Thr Gln
675 680 685
Val Val Gln Glu Arg Glu Ser Leu Leu Val Lys Ile Lys Val Leu Glu
690 695 700
Gln Asp Lys Ala Arg Leu Gln Arg Leu Glu Asp Glu Leu Asn Arg Ala
705 710 715 720
Lys Ser Thr Leu Glu Ala Glu Thr Arg Val Lys Gln Arg Leu Glu Cys
725 730 735
Glu Lys Gln Gln Ile Gln Asn Asp Leu Asn Gln Trp Lys Thr Gln Tyr
740 745 750
Ser Arg Lys Glu Glu Ala Ile Arg Lys Ile Glu Ser Glu Arg Glu Lys
755 760 765
Ser Glu Arg Glu Lys Asn Ser Leu Arg Ser Glu Ile Glu Arg Leu Gln
770 775 780
Ala Glu Ile Lys Arg Ile Glu Glu Arg Cys Arg Arg Lys Leu Glu Asp
785 790 795 800
Ser Thr Arg Glu Thr Gln Ser Gln Leu Glu Thr Glu Arg Ser Arg Tyr
805 810 815
Gln Arg Glu Ile Asp Lys Leu Arg Gln Arg Pro Tyr Gly Ser His Arg
820 825 830
Glu Thr Gln Thr Glu Cys Glu Trp Thr Val Asp Thr Ser Lys Leu Val
835 840 845

Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys
850 855 860
Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys
865 870 875 880
Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala
885 890 895
Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu
900 905 910
Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met
915 920 925
Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg
930 935 940
Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp
945 950 955 960
Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly
965 970 975
Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile
980 985 990
Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala
995 1000 1005
Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu
1010 1015 1020
Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr
1025 1030 1035 104
Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro
1045 1050 1055
Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg
1060 1065 1070
Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser
1075 1080 1085
Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
1090 1095 1100
Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly
1105 1110 1115 112
Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln
1125 1130 1135
Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys
1140 1145 1150
Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr
1155 1160 1165
Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp
1170 1175 1180
Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly
1185 1190 1195 120
Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala
1205 1210 1215
Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe
1220 1225 1230
Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu
1235 1240 1245
Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser
1250 1255 1260
His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu
1265 1270 1275 128
Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

1285 1290 1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu
1300 1305 1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys
1315 1320 1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys
1330 1335 1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val
1345 1350 1355 136
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu
1365 1370 1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser
1380 1385 1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln
1395 1400 1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe
1410 1415 1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp
1425 1430 1435 144
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser
1445 1450 1455
Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser
1460 1465 1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser
1475 1480 1485
Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe
1490 1495 1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg
1505 1510 1515 152
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala
1525 1530 1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu
1540 1545 1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser
1555 1560 1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly
1570 1575 1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro
1585 1590 1595 160
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly
1605 1610 1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile
1620 1625 1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr
1635 1640 1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile
1650 1655 1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly
1665 1670 1675 168
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser
1685 1690 1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser
1700 1705 1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg
1715 1720 1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser
    1730   1735   1740
Phe Ser Ser Ser Ser Ile Gly His
1745   1750

<210> 73
<211> 1978
<212> PRT
<213> Homo Sapiens

<400> 73
Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg
 1   5   10   15
Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met
            20   25   30
Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala
        35   40   45
Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met
    50   55   60
Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro
65   70   75   80
Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys
                85   90   95
Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala
            100   105   110
Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser
        115   120   125
Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu
    130   135   140
Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr
145   150   155   160
Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp
                165   170   175
Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln
            180   185   190
Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val
        195   200   205
Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu
    210   215   220
Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn
225   230   235   240
Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn
                245   250   255
Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met
            260   265   270
Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu
        275   280   285
Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val
    290   295   300
Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser
305   310   315   320
Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro
                325   330   335
Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro
            340   345   350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly
355 360 365

Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro
370 375 380

Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp
385 390 395 400

Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr
405 410 415

Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn
420 425 430

Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser
435 440 445

Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp
450 455 460

Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu
465 470 475 480

Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser
485 490 495

Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met
500 505 510

His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg
515 520 525

Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg
530 535 540

Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser
545 550 555 560

Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys
565 570 575

Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn
580 585 590

Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln
595 600 605

Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser
610 615 620

Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys
625 630 635 640

Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser
645 650 655

Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu
660 665 670

His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys
675 680 685

Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn
690 695 700

Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu
705 710 715 720

Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro
725 730 735

Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys
740 745 750

Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys
755 760 765

Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val
770 775 780

Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785 790 795 800
Cys Val Ala Lys Val Asn Lys Ser Thr Gly Lys Ser Ala Ser Ser Val
805 810 815
Lys Ser Val Val Thr Val Ala Val Lys Gly Asn Lys Ala Ser Ile Lys
820 825 830
Thr Ala Lys Ser Gly Gly Lys Lys Ser Leu Glu Ala Lys Lys Thr Gly
835 840 845
Asn Val Lys Asn Lys Asp Ser Asn Lys Pro Val Thr Ile Pro Glu Asn
850 855 860
Ser Glu Ile Lys Thr Ser Ile Glu Val Lys Ala Thr Glu Asn Cys Ala
865 870 875 880
Lys Glu Ala Ile Ser Asp Ala Ala Leu Glu Ala Thr Glu Asn Glu Pro
885 890 895
Leu Asn Lys Glu Thr Glu Glu Met Cys Val Met Leu Val Ser Asn Leu
900 905 910
Pro Asn Lys Gly Tyr Ser Val Glu Glu Val Tyr Asp Leu Ala Lys Pro
915 920 925
Phe Gly Gly Leu Lys Asp Ile Leu Ile Leu Ser Ser His Lys Lys Ala
930 935 940
Tyr Ile Glu Ile Asn Arg Lys Ala Ala Glu Ser Met Val Lys Phe Tyr
945 950 955 960
Thr Cys Phe Pro Val Leu Met Asp Gly Asn Gln Leu Ser Ile Ser Met
965 970 975
Ala Pro Glu Asn Met Asn Ile Lys Asp Glu Glu Ala Ile Phe Ile Thr
980 985 990
Leu Val Lys Glu Asn Asp Pro Glu Ala Asn Ile Asp Thr Ile Tyr Asp
995 1000 1005
Arg Phe Val His Leu Asp Asn Leu Pro Glu Asp Gly Leu Gln Cys Val
1010 1015 1020
Leu Cys Val Gly Leu Gln Phe Gly Lys Val Asp His His Val Phe Ile
1025 1030 1035 104
Ser Asn Arg Asn Lys Ala Ile Leu Gln Leu Asp Ser Pro Glu Ser Ala
1045 1050 1055
Gln Ser Met Tyr Ser Phe Leu Lys Gln Asn Pro Gln Asn Ile Gly Asp
1060 1065 1070
His Met Leu Thr Cys Ser Leu Ser Pro Lys Ile Asp Leu Pro Glu Val
1075 1080 1085
Gln Ile Glu His Asp Pro Glu Leu Glu Lys Glu Ser Pro Gly Leu Lys
1090 1095 1100
Asn Ser Pro Ile Asp Glu Ser Glu Val Gln Thr Ala Thr Asp Ser Pro
1105 1110 1115 112
Ser Val Lys Pro Asn Glu Leu Glu Glu Glu Ser Thr Pro Ser Ile Gln
1125 1130 1135
Thr Glu Thr Leu Val Gln Gln Glu Glu Pro Cys Glu Glu Glu Ala Glu
1140 1145 1150
Lys Ala Thr Cys Asp Ser Asp Phe Ala Val Glu Thr Leu Glu Leu Glu
1155 1160 1165
Thr Gln Gly Glu Glu Val Lys Glu Glu Ile Pro Leu Val Ala Ser Ala
1170 1175 1180
Ser Val Ser Ile Glu Gln Phe Thr Glu Asn Ala Glu Glu Cys Ala Leu
1185 1190 1195 120
Asn Gln Gln Met Phe Asn Ser Asp Leu Glu Lys Lys Gly Ala Glu Ile
1205 1210 1215
Ile Asn Pro Lys Thr Ala Leu Leu Pro Ser Asp Ser Val Phe Ala Glu
1220 1225 1230

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu
1235 1240 1245
Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu
1250 1255 1260
Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile
1265 1270 1275 128
Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp
1285 1290 1295
Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu
1300 1305 1310
Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr
1315 1320 1325
Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu
1330 1335 1340
Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys
1345 1350 1355 136
Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr
1365 1370 1375
Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro
1380 1385 1390
Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val
1395 1400 1405
Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp
1410 1415 1420
Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu
1425 1430 1435 144
Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe
1445 1450 1455
Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser
1460 1465 1470
Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys
1475 1480 1485
Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp
1490 1495 1500
Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser
1505 1510 1515 152
Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe
1525 1530 1535
Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn
1540 1545 1550
Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr
1555 1560 1565
Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Lys Gly
1570 1575 1580
Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr
1585 1590 1595 160
Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln
1605 1610 1615
Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met
1620 1625 1630
Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu
1635 1640 1645
Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr
1650 1655 1660
Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu

1665 1670 1675 168
Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu
1685 1690 1695
Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly
1700 1705 1710
Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu
1715 1720 1725
Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser
1730 1735 1740
Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp
1745 1750 1755 176
Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr
1765 1770 1775
Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val
1780 1785 1790
Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn
1795 1800 1805
Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu
1810 1815 1820
Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys
1825 1830 1835 184
Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val
1845 1850 1855
Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro
1860 1865 1870
Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser
1875 1880 1885
Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp
1890 1895 1900
Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp
1905 1910 1915 192
Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe
1925 1930 1935
Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His
1940 1945 1950
Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu
1955 1960 1965
Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg
1970 1975

<210> 74
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 74
Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15
Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
20 25 30
Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala
35 40 45
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
50 55 60
Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

65 70 75 80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
85 90 95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
100 105 110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
115 120 125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
130 135 140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145 150 155 160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
165 170 175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
180 185 190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
195 200 205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
210 215 220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225 230 235 240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
245 250 255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
260 265 270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
275 280 285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
290 295 300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
305 310 315 320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
325 330 335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
340 345 350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
355 360 365

<210> 75
<211> 240
<212> PRT
<213> Homo Sapiens

<400> 75
Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
1 5 10 15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
20 25 30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
35 40 45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
50 55 60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65 70 75 80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

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                85                  90                  95
Glu Tyr Leu Ala Trp Gln His Thr Thr Leu Arg Arg Ser Cys Leu Arg
            100                 105                 110
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Gly Pro Val
        115                 120                 125
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu
    130                 135                 140
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly
145                 150                 155                 160
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His
                165                 170                 175
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala
            180                 185                 190
Thr Trp Arg Gln Arg Val Glu Ala Ala Val Gly Glu Asp Leu Phe Gln
        195                 200                 205
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp
    210                 215                 220
Pro Thr Ile Lys Gln Lys Leu Met Pro Trp Val Leu Ala Met Ile Arg
225                 230                 235                 240

      <210> 76
      <211> 953
      <212> PRT
      <213> Homo Sapiens

      <400> 76
Met Ile Thr Ser Ala Ala Gly Ile Ile Ser Leu Leu Asp Glu Asp Glu
 1               5                  10                  15
Pro Gln Leu Lys Glu Phe Ala Leu His Lys Leu Asn Ala Val Val Asn
            20                  25                  30
Asp Phe Trp Ala Glu Ile Ser Glu Ser Val Asp Lys Ile Glu Val Leu
        35                  40                  45
Tyr Glu Asp Glu Gly Phe Arg Ser Arg Gln Phe Ala Ala Leu Val Ala
    50                  55                  60
Ser Lys Val Phe Tyr His Leu Gly Ala Phe Glu Glu Ser Leu Asn Tyr
65                  70                  75                  80
Ala Leu Gly Ala Arg Asp Leu Phe Asn Val Asn Asp Asn Ser Glu Tyr
                85                  90                  95
Val Glu Thr Ile Ile Ala Lys Cys Ile Asp His Tyr Thr Lys Gln Cys
            100                 105                 110
Val Glu Asn Ala Asp Leu Pro Glu Gly Glu Lys Lys Pro Ile Asp Gln
        115                 120                 125
Arg Leu Glu Gly Ile Val Asn Lys Met Phe Gln Arg Cys Leu Asp Asp
    130                 135                 140
His Lys Tyr Lys Gln Ala Ile Gly Ile Ala Leu Glu Thr Arg Arg Leu
145                 150                 155                 160
Asp Val Phe Glu Lys Thr Ile Leu Glu Ser Asn Asp Val Pro Gly Met
                165                 170                 175
Leu Ala Tyr Ser Leu Lys Leu Cys Met Ser Leu Met Gln Asn Lys Gln
            180                 185                 190
Phe Arg Asn Lys Val Leu Arg Val Leu Val Lys Ile Tyr Met Asn Leu
        195                 200                 205
Glu Lys Pro Asp Phe Ile Asn Val Cys Gln Cys Leu Ile Phe Leu Asp
    210                 215                 220
Asp Pro Gln Ala Val Ser Asp Ile Leu Glu Lys Leu Val Lys Glu Asp
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225                 230                 235                 240
Asn Leu Leu Met Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala
                245                 250                 255
Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly
            260                 265                 270
Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro
        275                 280                 285
Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser
    290                 295                 300
Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp
305                 310                 315                 320
Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu
                325                 330                 335
Leu His Leu Gln Phe Leu Ile Arg Asn Asn Asn Thr Asp Leu Met Ile
            340                 345                 350
Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala
        355                 360                 365
Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln
    370                 375                 380
Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala
385                 390                 395                 400
Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu
                405                 410                 415
Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser
            420                 425                 430
Pro Gly Ser Ala Tyr Gln Glu Gly Gly Gly Leu Tyr Ala Leu Gly Leu
        435                 440                 445
Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln
    450                 455                 460
Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly
465                 470                 475                 480
Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu
                485                 490                 495
Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala
            500                 505                 510
Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala
        515                 520                 525
Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile
    530                 535                 540
Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met
545                 550                 555                 560
Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro
                565                 570                 575
Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly
            580                 585                 590
Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser
        595                 600                 605
Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe
    610                 615                 620
Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu
625                 630                 635                 640
Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu
                645                 650                 655
Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu
            660                 665                 670
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Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu
675 680 685
Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro
690 695 700
Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys
705 710 715 720
His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile
725 730 735
Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr
740 745 750
Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln
755 760 765
Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr
770 775 780
Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val
785 790 795 800
Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro
805 810 815
Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val
820 825 830
Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys
835 840 845
Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu
850 855 860
Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn
865 870 875 880
Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu
885 890 895
Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile
900 905 910
Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val
915 920 925
Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro
930 935 940
Pro Glu Pro Phe Glu Tyr Ile Asp Asp
945 950

<210> 77
<211> 335
<212> PRT
<213> Homo Sapiens

<400> 77
Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
1 5 10 15
Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
20 25 30
Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
35 40 45
Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn
50 55 60
Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
65 70 75 80
Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
100 105 110
Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala
115 120 125
Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu
130 135 140
Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
145 150 155 160
Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
165 170 175
Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
180 185 190
Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro
195 200 205
Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
210 215 220
Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val
225 230 235 240
Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
245 250 255
Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly
260 265 270
Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser
275 280 285
Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
290 295 300
Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr
305 310 315 320
Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu
325 330 335

<210> 78
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 78
Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala
1 5 10 15
Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr
20 25 30
Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val
35 40 45
Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu
50 55 60
Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly
65 70 75 80
Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu
85 90 95
Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln
100 105 110
Ser Gln Lys Ala Lys
115

<210> 79

<211> 614
<212> PRT
<213> Homo Sapiens

<400> 79
Arg Ser Gly Gln Pro Arg Ala Glu Gly Leu Gly Ala Gly Ala Ala Gly
1 5 10 15
Pro Leu Arg Ala Met Ala Ala Pro Val Lys Gly Asn Arg Lys Gln Ser
20 25 30
Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro Lys Pro Ala Gly
35 40 45
Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu Asp Ser Pro Glu
50 55 60
Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu Glu Glu Gln Ala
65 70 75 80
Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg His Thr Pro Ile
85 90 95
Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn Leu Trp Lys Ile
100 105 110
Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu Val Thr Gly Arg
115 120 125
Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly Ser Pro Gly Ser
130 135 140
Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu Arg Leu Val Leu
145 150 155 160
Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys Pro Leu Pro Thr
165 170 175
Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu Asn Arg Gly Asp
180 185 190
Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu Glu Arg Arg Met
195 200 205
Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala Ala Asp Pro Ala
210 215 220
Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr Glu Gln Gln Gly
225 230 235 240
Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala Ser Gly Cys Pro
245 250 255
Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys Lys Gly Thr His
260 265 270
Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu Ala Gln Val Ser
275 280 285
Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys Arg His Gly Ala
290 295 300
Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu Ser Pro Gln Ser
305 310 315 320
Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu Thr Pro Gln Glu
325 330 335
Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu Ala Gln Ala Gly
340 345 350
Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe Tyr Thr His Pro
355 360 365
Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg Asp Phe Phe Ser
370 375 380
Arg Leu Lys Asp Gly Val Leu Leu Gly Pro Pro Gly Lys Glu Gly Leu
385 390 395 400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro
405 410 415
Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys
420 425 430
Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser
435 440 445
Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys
450 455 460
Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg
465 470 475 480
Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala
485 490 495
Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu
500 505 510
Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro
515 520 525
Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu
530 535 540
Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala
545 550 555 560
Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro
565 570 575
Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser
580 585 590
Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe
595 600 605
His Leu Asn Thr Lys Leu
610

<210> 80
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 80
Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu
1 5 10 15
His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile
20 25 30
Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala
35 40 45
Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly
50 55 60
Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro
65 70 75 80
Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala
85 90 95
Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu
100 105 110
Phe Asp

<210> 81
<211> 596
<212> PRT

<213> Homo Sapiens

<400> 81

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Met Arg Arg Ala His Glu Gly Arg Glu Ile Pro Ser Leu Gly Gly Ala
1               5                   10                  15
Arg Arg Arg Glu Val Leu Gln Ala Gly Arg Ser Gln Arg Ala Ala Gly
            20                  25                  30
Arg Arg Arg Arg Arg Gln Glu Leu Glu Leu Gly Val Gly Ser Gly Arg
        35                  40                  45
Pro Gly Gly Pro Pro Pro Gly Pro Gly Arg Arg Gly Thr Cys Ala Ala
    50                  55                  60
Ala Leu Pro Pro Glu Trp Pro Arg Arg Arg Thr Gly Leu Pro Arg Arg
65                  70                  75                  80
Gly Pro Arg Pro Pro Leu Ala Met Ala Lys Trp Leu Asn Lys Tyr Phe
                85                  90                  95
Ser Leu Gly Asn Ser Lys Thr Lys Ser Pro Pro Gln Pro Pro Arg Pro
            100                 105                 110
Asp Tyr Arg Glu Gln Arg Arg Arg Gly Glu Arg Pro Ser Gln Pro Pro
        115                 120                 125
Gln Ala Val Pro Gln Ala Ser Ser Ala Ala Ser Ala Ser Cys Gly Pro
    130                 135                 140
Ala Thr Ala Ser Cys Phe Ser Ala Ser Ser Gly Ser Leu Pro Asp Asp
145                 150                 155                 160
Ser Gly Ser Thr Ser Asp Leu Ile Arg Ala Tyr Arg Ala Gln Lys Glu
                165                 170                 175
Arg His Phe Gln Asp Pro Tyr Asn Gly Pro Gly Ser Ser Leu Arg Lys
            180                 185                 190
Leu Arg Ala Met Cys Arg Leu Asp Tyr Cys Gly Gly Ser Gly Glu Pro
        195                 200                 205
Gly Gly Val Gln Arg Ala Phe Ser Ala Ser Ser Ala Ser Gly Ala Ala
    210                 215                 220
Gly Cys Cys Cys Ala Ser Ser Gly Ala Gly Ala Ala Ala Ser Ser Ser
225                 230                 235                 240
Ser Ser Ser Gly Ser Pro His Leu Tyr Arg Ser Ser Ser Glu Arg Arg
                245                 250                 255
Pro Ala Thr Pro Ala Glu Val Arg Tyr Ile Ser Pro Lys His Arg Leu
            260                 265                 270
Ile Lys Val Glu Ser Ala Ala Gly Gly Gly Ala Gly Asp Pro Leu Gly
        275                 280                 285
Gly Ala Cys Ala Gly Gly Arg Thr Trp Ser Pro Thr Ala Cys Gly Gly
    290                 295                 300
Lys Lys Leu Leu Asn Lys Cys Ala Ala Ser Ala Ala Glu Glu Ser Gly
305                 310                 315                 320
Ala Gly Lys Lys Asp Lys Val Thr Ile Ala Asp Asp Tyr Ser Asp Pro
                325                 330                 335
Phe Asp Ala Lys Asn Asp Leu Lys Ser Lys Ala Gly Lys Gly Glu Ser
            340                 345                 350
Ala Gly Tyr Met Glu Pro Tyr Glu Ala Gln Arg Ile Met Thr Glu Phe
        355                 360                 365
Gln Arg Gln Glu Ser Val Arg Ser Gln His Lys Gly Ile Gln Leu Tyr
    370                 375                 380
Asp Thr Pro Tyr Glu Pro Glu Gly Gln Ser Val Asp Ser Asp Ser Glu
385                 390                 395                 400
Ser Thr Val Ser Pro Arg Leu Arg Glu Ser Lys Leu Pro Gln Asp Asp
                405                 410                 415
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Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val
420 425 430
Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln
435 440 445
Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Arg Gln Leu Arg Ala Pro
450 455 460
Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly
465 470 475 480
Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile
485 490 495
Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg
500 505 510
Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys
515 520 525
His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met
530 535 540
Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro
545 550 555 560
Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys
565 570 575
Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala
580 585 590
Val Arg Thr Leu
595

<210> 82
<211> 207
<212> PRT
<213> Homo Sapiens

<400> 82
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
130 135 140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145 150 155 160
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
165 170 175
His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
195 200 205

<210> 83
<211> 429
<212> PRT
<213> Homo Sapiens

<400> 83
Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp
1 5 10 15
Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser
20 25 30
Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val
35 40 45
Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser
50 55 60
Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr
65 70 75 80
Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser
85 90 95
Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp
100 105 110
Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser
115 120 125
Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg
130 135 140
His Asp Pro Arg Asp Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg
145 150 155 160
Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys
165 170 175
His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln
180 185 190
Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile
195 200 205
Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro
210 215 220
Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg
225 230 235 240
Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu
245 250 255
Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg
260 265 270
Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala
275 280 285
Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu
290 295 300
Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr
305 310 315 320
Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn
325 330 335
Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu
340 345 350
Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His
355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu
370 375 380
Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu
385 390 395 400
Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala
405 410 415
Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys
420 425

<210> 84
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 84
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
1 5 10 15
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
20 25 30
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
35 40 45
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
50 55 60
Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln
65 70 75 80
Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp
85 90 95
Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val
100 105 110
Gly

<210> 85
<211> 258
<212> PRT
<213> Homo Sapiens

<400> 85
Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly
1 5 10 15
Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu
20 25 30
Ala His Ser Gln Ile Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe
35 40 45
Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg
50 55 60
Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys
65 70 75 80
Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro
85 90 95
Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala
100 105 110
Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe
115 120 125
Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140
Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys
145 150 155 160
Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu
165 170 175
Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly
180 185 190
Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met
195 200 205
Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser
210 215 220
Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His
225 230 235 240
Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile
245 250 255
Val Leu

<210> 86
<211> 569
<212> PRT
<213> Homo Sapiens

<400> 86
Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
1 5 10 15
Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
20 25 30
Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
35 40 45
Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
50 55 60
Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
65 70 75 80
Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
85 90 95
Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
100 105 110
Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
115 120 125
Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
130 135 140
Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
145 150 155 160
Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
165 170 175
Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
180 185 190
Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
195 200 205
Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
210 215 220
Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
225 230 235 240
Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

245 250 255
Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
260 265 270
Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
275 280 285
His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
290 295 300
Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
305 310 315 320
Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
325 330 335
Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
340 345 350
Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
355 360 365
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
370 375 380
Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
385 390 395 400
Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
405 410 415
Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
420 425 430
Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
435 440 445
Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys
450 455 460
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
465 470 475 480
Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn
485 490 495
Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met
500 505 510
Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr
515 520 525
Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp
530 535 540
Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln
545 550 555 560
Gln Gln Trp Pro Gly Arg Arg His Arg
565

<210> 87
<211> 736
<212> PRT
<213> Homo Sapiens

<400> 87
Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn
1 5 10 15
Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly
20 25 30
Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg
35 40 45
Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

50 55 60
Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly
65 70 75 80
Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr
85 90 95
Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu
100 105 110
Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu
115 120 125
Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu
130 135 140
Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys
145 150 155 160
Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn
165 170 175
Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala
180 185 190
Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg
195 200 205
Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr
210 215 220
Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly
225 230 235 240
Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys
245 250 255
Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys
260 265 270
Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr
275 280 285
Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu
290 295 300
Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn
305 310 315 320
Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu
325 330 335
Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala
340 345 350
Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr
355 360 365
Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu
370 375 380
Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr
385 390 395 400
Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu
405 410 415
Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val
420 425 430
Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn
435 440 445
Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile
450 455 460
Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn
465 470 475 480
Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr
485 490 495

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Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile
            500                 505                 510
Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val
        515                 520                 525
Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser
    530                 535                 540
Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile
545                 550                 555                 560
Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly
                565                 570                 575
Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met
            580                 585                 590
Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys
        595                 600                 605
Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn
    610                 615                 620
Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu
625                 630                 635                 640
Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu
                645                 650                 655
Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His
            660                 665                 670
Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly
        675                 680                 685
Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu
    690                 695                 700
Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu
705                 710                 715                 720
Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp
                725                 730                 735

      <210> 88
      <211> 37
      <212> PRT
      <213> Homo Sapiens

      <400> 88
Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly
 1               5                  10                  15
Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
            20                  25                  30
Lys Leu Leu Leu Gln
        35

      <210> 89
      <211> 1381
      <212> DNA
      <213> Homo Sapiens

      <400> 89
ccgcagccct agagccgccc aagggatggc gatggcgtac ttggcttgga gactggcgcg      60
gcgttcgtgt ccgagttctc tgcaggtcnc tantttcccg gtagttcanc tgcncatgaa     120
tanaacagca atgagagccn ctcncaaaga ctttgaaaat tcactgaatc nagtgaaact     180
ctngaaaaag gatccangaa acgaaatgaa nctnaaactc tncgcgctat atnancangc     240
cnctgaanga cttgtntcat gcccnaacca ngtgtntttg acttgatcna caaggggcca     300
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atgggacaca tggaatgccc ttggcancct gcccnaagaa ctgccaggca naactatgtg     360
gatttggtgt ccantttgan tccntccttg gaatcctcna atcnngtgga ncctggaaca     420
nacaggaaat ccactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaaag     480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt     540
atgcgtgcac ttaaagctgc cagcaaggat gactcaatca tcactgtttt aacaggaaat     600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctggtgga     660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttgtggg ctgttttata     720
gattttccta agcctctgat tgcagtggtc aatggtccag ctgtgggcat ctccgtcacc     780
ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt     840
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc     900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt     960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc    1020
aggctgaagg catttgcaaa gcttcccccca aatgccttga gaatttcaaa agaggtaatc   1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag    1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttatc cagaaaatca    1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct    1260
ctgatttcca gtactggaac taaataagct tcattgtgcc ttttgtagtg ctagaatatc    1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa    1380
a                                                                    1381
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<210> 90
<211> 298
<212> PRT
<213> Homo Sapiens

<400> 90

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Thr Cys Met Pro Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
 1               5                  10                  15
Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
            20                  25                  30
Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
        35                  40                  45
Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
    50                  55                  60
Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
65                  70                  75                  80
Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
                85                  90                  95
Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
            100                 105                 110
Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
        115                 120                 125
Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
    130                 135                 140
Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
145                 150                 155                 160
Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
                165                 170                 175
Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
            180                 185                 190
Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
        195                 200                 205
Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
    210                 215                 220
Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys
```

225 230 235 240
Glu Val Trp Thr Lys Leu Lys Ala Phe Ala Lys Ala Ser Pro Lys Cys
245 250 255
Leu Glu Asn Phe Lys Arg Gly Asn Gln Gly Lys Glu Arg Glu Lys Asn
260 265 270
Tyr Thr Pro Leu Met Leu Lys Lys Cys Asn Val Pro Ser Arg Lys Gly
275 280 285
Tyr Gln Asp Glu Cys Thr Lys Cys Leu Trp
290 295

<210> 91
<211> 1514
<212> DNA
<213> Homo Sapiens

<400> 91
gccgcgcgct gtgtctccgc tgcgtccgcc gaggcccccg agtgtcaggg acaaaagcct 60
ccgcctgctc ccgcagccgg ggctcatctg ccgccgccgc cgcgctgagg agagttcgcc 120
gccgtcgccg cccgtgagga tctgagagcc atgtcggcca gcagcctctt ggagcagaga 180
ccaaaaggtc aaggaaacaa agtacaaaat ggatctgtac atcaaaagga tggattaaac 240
gatgatgatt ttgaacctta cttgagtcca caggcaaggc ccaataatgc atatactgcc 300
atgtcagatt cctacttacc cagttactac agtccctcca ttggcttctc ctattctttg 360
ggtgaagctg cttggtctac ggggggtgac acagccatgc cctacttaac ttcttatgga 420
cagctgagca acggagagcc ccacttccta ccagatgcaa tgtttgggca accaggagcc 480
ctaggtagca ctccatttct tggtcagcat ggttttaatt tctttcccag tgggattgac 540
ttctcagcat ggggaaataa cagttctcag ggacagtcta ctcagagctc tggatatagt 600
agcaattatg cttatgcacc tagctcctta ggtggagcca tgattgatgg acagtcagct 660
tttgccaatg agaccctcaa taaggctcct ggcatgaata ctatagacca agggatggca 720
gcactgaagt tgggtagcac agaagttgca agcaatgttc caaaagttgt aggttctgct 780
gttggtagcg ggtccattac tagtaacatc gtggcttcca atagtttgcc tccagccacc 840
attgctcctc caaaaccagc atcttgggct gatattgcta gcaagcctgc aaaacagcaa 900
cctaaactga agaccaagaa tggcattgca gggtcaagtc ttccgccacc cccgataaag 960
cataacatgg atattggaac ttgggataac aagggtcccg ttgcaaaagc cccctcacag 1020
gctttggttc agaatatagg tcagccaacc caggggtctc ctcagcctgt aggtcagcag 1080
gctaacaata gcccaccagt ggctcaggca tcagtagggc aacagacaca gccattgcct 1140
ccacctccac cacagcctgc ccagctttca gtccagcaac aggcagctca gccaacccgc 1200
tgggtagcac ctcggaaccg tggcagtggg ttcggtcata atggggtgga tggtaatgga 1260
gtaggacagt ctcaggctgg ttctggatct actccttcag aaccccaccc agtgttggag 1320
aagcttcggt ccattaataa ctataacccc aaagatttg actgggaaat ctgaaacatg 1380
ggcgggtttt catcattaaa gaactactct gangacgata ttcaccgttc catttaagtt 1440
ataatatttg gtggancaca anagcaatgg taacaagaga atgggatgcc ngcttatcgt 1500
ttccatgaac gggg 1514

<210> 92
<211> 407
<212> PRT
<213> Homo Sapiens

<400> 92
Met Ser Ala Ser Ser Leu Leu Glu Gln Arg Pro Lys Gly Gln Gly Asn
1 5 10 15
Lys Val Gln Asn Gly Ser Val His Gln Lys Asp Gly Leu Asn Asp Asp
20 25 30
Asp Phe Glu Pro Tyr Leu Ser Pro Gln Ala Arg Pro Asn Asn Ala Tyr
35 40 45

```
Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile
    50                  55                  60
Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp
65                  70                  75                  80
Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu
                85                  90                  95
Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly
            100                 105                 110
Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly
        115                 120                 125
Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr
    130                 135                 140
Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu
145                 150                 155                 160
Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu
                165                 170                 175
Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu
            180                 185                 190
Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly
        195                 200                 205
Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn
    210                 215                 220
Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala
225                 230                 235                 240
Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys
                245                 250                 255
Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn
            260                 265                 270
Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro
        275                 280                 285
Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro
    290                 295                 300
Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala
305                 310                 315                 320
Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Pro Gln Pro
                325                 330                 335
Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val
            340                 345                 350
Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly
        355                 360                 365
Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu
    370                 375                 380
Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro
385                 390                 395                 400
Lys Asp Phe Asp Trp Glu Ile
                405
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<210> 93
<211> 2236
<212> DNA
<213> Homo Sapiens

<400> 93

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cctggcccgg tcgcggtcgc ggctctttcc agctcctggc agccgggcac ccgaaggaac      60
gggtcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggcccgagaa     120
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ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat    180
gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg    240
gtcatcaatg aacccagccg tctgcctctg tttgatgcca ttcggccgct gatcccactg    300
aagcaccagg tggaatatga tcagctgacc ccccggcgct ccaggaagct gaaggaggtg    360
cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt    420
ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc    480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg tacccatgag    540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagtgag acacatcggc    600
ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt    660
gtgtcggaat ctgggggcgt gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag    720
gagaagaagg tcttcatcag cctggtaggc tcccgaggcc ttggctgcag catttccagc    780
ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct    840
gaggtgggat tggagatagg ggaccagatt gtcgaagtca atggcgtcga cttctctaac    900
ctggatcaca aggaggctgt aaatgtgctg aaaaatagcc gcagcctgac catctccatt    960
gtagctgcag ctggccggga gctgttcatg acagaccggg agcggctggc agaggcgcgg   1020
cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac   1080
aagatcctcc aggagcagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag   1140
gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag   1200
aagtttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa   1260
accatcactg ctgaggtaca cccagtaccc cttcgcaagc caaagtatga tcagggagtg   1320
gaacctgagc tcgagcccgc agatgacctg gatggaggca cggaggagca gggagagcag   1380
gatttccgga aatatgagga aggctttgac ccctactcta tgttcacccc agagcagatc   1440
atggggaagg atgtccggct cctacgcatc aagaaggagg gatccttaga cctggccctg   1500
gaaggcggtg tggactcccc cattgggaag gtggtcgttt ctgctgtgta tgagcgggga   1560
gctgctgagc ggcatggtgg cattgtgaaa ggggacgaga tcatggcaat caacggcaag   1620
attgtgacag actacaccct ggctgaggct gacgctgccc tgcagaaggc ctggaatcag   1680
ggcggggact ggatcgacct tgtggttgcc gtctgccccc caaaggagta tgacgatgag   1740
ctgaccttct tgctgaagtc caaaagggga aaccaaattc acgcgttagg aaacagtgag   1800
ctccggcccc acctcgtgaa cacaaagcct cggaccagcc ttgagagagg ccacatgaca   1860
cacaccagat ggcatccttg ggacctgaat ctatcaccca ggaatctcaa actccctttg   1920
gccctgaacc agggccagat aaggaacagc tcgggccact tttttgaagg ccaatgtgga   1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt   2040
cctctggccc agtgaatttg gtctctccca gctttggggg actccttcct tgaaccctaa   2100
taagacccca ctggagtctc tctctctcca tccctctcct ctgccctctg ctctaattgc   2160
tgccaggatt gtcactccaa accttactct gagctcatta ataaaataaa cagatttatt   2220
ttccagctta aaaaaa                                                   2236
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<210> 94
<211> 652
<212> PRT
<213> Homo Sapiens

<400> 94

```
Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1               5                  10                  15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
            20                  25                  30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
        35                  40                  45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
    50                  55                  60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65                  70                  75                  80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
                85                  90                  95
```

Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100 105 110

Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115 120 125

Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130 135 140

Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145 150 155 160

Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165 170 175

Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180 185 190

Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195 200 205

Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210 215 220

Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225 230 235 240

Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245 250 255

Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
260 265 270

Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
275 280 285

Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
290 295 300

Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305 310 315 320

Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
325 330 335

Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
340 345 350

Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
355 360 365

Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
370 375 380

Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385 390 395 400

Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
405 410 415

Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
420 425 430

Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
435 440 445

Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
450 455 460

Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
465 470 475 480

Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
485 490 495

Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
500 505 510

Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
515 520 525

Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

```
    530                 535                 540
Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
545                 550                 555                 560
Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
                565                 570                 575
Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
            580                 585                 590
His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
        595                 600                 605
Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
    610                 615                 620
Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
625                 630                 635                 640
Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
                645                 650
```

<210> 95
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 95

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cataactggg actcgcgcgc ctgcaggtcg acactagtgg gatccaaaga attcggcacg      60
agaaaccaca atgcccagat ctcaagtaga tgaagagttt ttgaagcaaa gtttaaagga     120
aaaacnattg cagaaaacat ttagattnta tgaaatatat aatnanancc aaaanccatt     180
tgaanttaat nganccttac ctgtcntcac taaatcaggg ttntctgcgc caccnaaggg     240
cngcccancg cctgctgtgt tggcttanta ggcctnagca tangggcagn tgcaatcctt     300
tcctcctnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgcaaggc     360
ggcccctccc ctgccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga     420
agggtggact ggctatcntg gaagatcaga taccaccaag caatttggag acagttcctg     480
ttgagaataa ccacggtttc catgaaaaga cagcagcgct gaagcttgag gccgagggcg     540
aggccatgga agatgcagcc gcgccaggga acgaccgagg cggcacacag gagccagccc     600
cagtgcctgc tgagccgttt gacaacacta cctacaagaa cctgcagcat catgactaca     660
gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct     720
cctcaggccg ggagtcacct cgacactgag ggccctcggt gtgaagatga accttccacc     780
gtcttcactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a              831
```

<210> 96
<211> 184
<212> PRT
<213> Homo Sapiens

<400> 96

```
Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu
 1               5                  10                  15
Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala
            20                  25                  30
Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu
        35                  40                  45
Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro
    50                  55                  60
Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu
65                  70                  75                  80
Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val
                85                  90                  95
```

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu
100 105 110
Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg
115 120 125
Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn
130 135 140
Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe
145 150 155 160
Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser
165 170 175
Ser Gly Arg Glu Ser Pro Arg His
180

<210> 97
<211> 1008
<212> DNA
<213> Homo Sapiens

<400> 97
gcaaggtctc caagtcccag ctcaaggtcc tttcccataa cctgtgcacg gtgctgaagg 60
ttcctcatga cccagttgcc cttgaagagc acttcaggga tgatgatgag ggtccagtgt 120
ccaaccaggg ctacatgcct tatttaaaca ggttcatttt ggaaaaggtc caagacaact 180
ttgacaagat tgaattcaat aggatgtgtt ggaccctctg tgtcaaaaaa aacctcacaa 240
agaatcccct gctcattaca gaagaanatg catttaaaat atgggttatt ttcaactttt 300
tatctgagga caagtatcca ttaattattg tgtcagaana gattgaatac ctgcttaaga 360
agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420
actttgatga cagtaaaaat ggcctttctg catgggaact tattgagctt attggaaatg 480
gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540
atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggc cacagacgga 600
aaaactggac tgaacgatgg tttgtactaa aacccaacat aatttcttac tatgtgagtg 660
aggatctgaa ggataagaaa ggagacattc tcttggatga aaattgctgt gtagagtcct 720
tgcctgacaa agatggaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780
aaatcagtgc ttcagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840
ttcatctgtt gaagctgngc agccctccac canacaaaga agccnnccag cttctnaaan 900
aactccggna gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960
aagcccgcca atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98
<211> 312
<212> PRT
<213> Homo Sapiens

<400> 98
Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr
1 5 10 15
Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg
20 25 30
Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu
35 40 45
Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu
50 55 60
Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys
65 70 75 80
Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe
85 90 95

```
Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile
            100                 105                 110
Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln
        115                 120                 125
Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn
    130                 135                 140
Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe
145                 150                 155                 160
Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val
                165                 170                 175
Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys
            180                 185                 190
Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys
        195                 200                 205
Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys
    210                 215                 220
Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp
225                 230                 235                 240
Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr
                245                 250                 255
Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile
            260                 265                 270
His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala
        275                 280                 285
Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg
    290                 295                 300
Gln Met Glu Leu Gln Ala Arg Gln
305                 310
```

<210> 99
<211> 1009
<212> DNA
<213> Homo Sapiens

<400> 99

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ggctaatgta acatactcta ccacttggtc tgaagcccag cagtatctga tggataatcc     60
aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt    120
tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgct    180
gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt    240
acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag    300
ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt    360
caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga    420
cattctaaag gataaaggat ttgtagttga agtaaacact actttgaag atttgtggc      480
gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt    540
caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg    600
gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctcctccgat    660
agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga    720
ggacataact ctagaatctg aaagaaaacg aatatttaaa gattttatgc atgtgcttga    780
gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca    840
tcataggaaa cgttcccgct ctcgatcggg gtcagattca ngatgatgat gatagccatt    900
caaagaaaaa aagacagcga tgagaagtct cggtctgntt canaacattc ttccantngc    960
agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagtt               1009
```

<210> 100
<211> 292

<212> PRT
<213> Homo Sapiens

<400> 100
Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu
1 5 10 15
Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp
20 25 30
Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu
35 40 45
Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg
50 55 60
Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu
65 70 75 80
His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr
85 90 95
Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro
100 105 110
Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys
115 120 125
Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp
130 135 140
Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala
145 150 155 160
Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile
165 170 175
Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg
180 185 190
Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala
195 200 205
Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala
210 215 220
Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu
225 230 235 240
Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met
245 250 255
His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys
260 265 270
His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg
275 280 285
Ser Gly Ser Asp
290

<210> 101
<211> 983
<212> DNA
<213> Homo Sapiens

<400> 101
aggtgacaat agatatagaa gtacgttgat gtgcgaagat gtattttgtt ttagccagcg 60
aggaaaaaag aatcagtttg attatacatt taccaaacat taagaattta atatggtaac 120
ttttatttca gtattaaaat agcaatttta tttattactt ttttatatat agaatttgac 180
accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240
acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300
cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

```
gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc     420
gtgacgaagg ctccttgggc aagccattgt gtccacccga gatactctcg gagacgttgc     480
caggctctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag     540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag     600
gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct     660
ctgaggaagc cacagaagtt cacatgatgg agggggaccc agacacactg gccgaacttc     720
tgatcaggga tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg     780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg     840
tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggacccag     900
ccacgctggc aaagagtgac ctggaagacc tggaggagca tgtgccagag cagacagtct     960
ctgaggaagc cacaggggtt cac                                             983
```

<210> 102
<211> 230
<212> PRT
<213> Homo Sapiens

<400> 102

```
Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
1               5                   10                  15
Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
            20                  25                  30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
        35                  40                  45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
    50                  55                  60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
65                  70                  75                  80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
                85                  90                  95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
            100                 105                 110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
        115                 120                 125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
    130                 135                 140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
145                 150                 155                 160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
                165                 170                 175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
            180                 185                 190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
        195                 200                 205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
    210                 215                 220
Glu Ala Thr Gly Val His
225                 230
```

<210> 103
<211> 843
<212> DNA
<213> Homo Sapiens

<400> 103

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aatncccgct gcaggtcgac actagtggat ccaaagaatt cggcacgagg caagttctgg   60
gagctggaca cggaccacga cctgctcatc gacgcggacg acctggcgcg gcacaatgac  120
cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga  180
aaagtgcaga aggaagggaa gatcagctat gccgactttg tctggttttt gatctctgag  240
gaagacaaaa aaacaccgac cagcatcgag tactggttcc gctgcatgga cctggacggg  300
gacggcgccc tgtccatgtt cgagctcgag tacttctacg aggagcagtg ccgaaggctg  360
gacagcatgg ccatcgaggc cctgcccttc caggactgcc tctgccagat gctggacctg  420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc  480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag  540
cagatctccc tgctcaggga cggtgacagc ggcgggcccg agctctcgga ctgggagaag  600
tnccggccga agagtncgac atcctggtgg ccgangaaac cgtggggana ncccctgggga  660
agacgggttc naaggcgaac tcacccccnt gganCanaaa ctgantgcgc tgcgctcccc  720
gctgggccan aggccttctt ccaagcgcct cccgctgggg cgccgtggaa ctgttncaaa  780
ttcccctgcg gggacaagaa cttgaaaccg ctgtganncc ccccncnana acccnccccg  840
gnt                                                                843
```

<210> 104
<211> 197
<212> PRT
<213> Homo Sapiens

<400> 104

```
Arg Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Arg Gly Lys
1               5                   10                  15
Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
            20                  25                  30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
        35                  40                  45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
    50                  55                  60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
65                  70                  75                  80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
                85                  90                  95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
            100                 105                 110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
        115                 120                 125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
    130                 135                 140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
145                 150                 155                 160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
                165                 170                 175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
            180                 185                 190
Ser Asp Trp Glu Lys
        195
```

<210> 105
<211> 2264
<212> DNA
<213> Homo Sapiens

<400> 105

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ctagcacaag tacacaggcc ccagccgctt cccctactgg tgtagttcct ggtaccaaat     60
atgcagtacc tgacacgtcc acttaccagt atgatgaatc ttcaggatat tactatgatc    120
cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgacccagc    180
agtaccttta ctgggatggg gaaaaagaga cctacgtgcc agctgcagag tctagctccc    240
accagcagtc gggcctgcct cctgcaaaag aggggaaaga gaagaaggag aaacccaaga    300
gcaaaacagc ccagcagatt gccaaagaca tggaacgctg ggctaagagt ttgaataagc    360
agaaagaaaa ctttaaaaat agctttcagc ctgtcaattc cttgagggaa gaagaaagga    420
gagaatctgc tgcagcagac gctggctttg ctctctttga gaagaaggga gccttagctg    480
aaaggcagca gctcatccca gaattggtgc gaaatggaga tgaggagaat cccctcaaaa    540
ggggtctggt tgctgcttac agtggtgaca gtgacaatga ggaggagctg gtggagagac    600
ttgagagtga ggaagagaag ctagctgact ggaagaagat ggcctgtctg ctctgccggc    660
gccagttccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc    720
aaaacatgga catctaccga cgatccaggc tgagcgagca ggagctggaa gccttggagc    780
taagggagag agagatgaaa taccgagacc gagctgcaga aagacgggag aagtacggca    840
ttccagaacc tccagagccc aagcgcaaga agcagtttga tgccggcact gtgaattacg    900
agcaacccac caaagatggc attgaccaca gtaacattgg caacaagatg ctgcaggcca    960
tgggctggcg ggaaggctct ggcttgggac gaaagtgtca aggcattacg gctcccattg   1020
aggctcaagt tcggctaaag ggagctggcc taggagccaa aggcagcgca tatggtttgt   1080
cgggcgccga ttcctacaaa gatgctgtcc ggaaagccat gtttgcccgg ttcactgaga   1140
tggagtgaga gagagagaga gagagagatg acaaggagca caagaagtgg tccatctccc   1200
gaattcgctg ttaccgcctg tctctttaag ggcatgcctt gtgctgttaa tagatcttag   1260
ggtgaaccac ttcattctgc agggttctcc ctcccacctt aaagaagttc cccttatgtg   1320
ggttgcctgg tgaatggcct tccttcccgc cagagggctt gtgaacagac cggagaggac   1380
agtggattgt ttatactcca gtgtacatag tgtaatgtag cgtgtttaca tgtgtagcct   1440
atgttgtggt ccatcagccc ctcacattcc taggggtttg agatgctgta ggtggtatgt   1500
gacaccaaag ccacctctgt catttgttgt gatgtctttt cttggcaaaa gccttgtgta   1560
tatttgtata ttacacattt gtacagaatt ttggaagatt ttcaatccaa gttgccaaat   1620
ctggctcctt tacaaaagaa ataccttgag aaaaaaaann aannaaaaaa aannccccnan   1680
nnnttttttaa aangggncgg gggccaannn ttttccnncc ggggngggna nnaagtaaan   1740
ngtcccaaat ncccccaaaa nggagcccnn ttaaaattaa angggccgcn nttttaaaan   1800
nttcngaatn gggnaaaccc tnggggtttn ccaaatttaa cccctttgaa aaaaaanccc   1860
ctttcncaaa annggggntaa tanccaaaaa gggcccccan ccatttttgc ccnttccaaa   1920
aaaatttgnc caanccnnaa atgggnaaan ggggaatcca atttttttaaa gggnnaaaan   1980
gggtttaaac nnacgggntt ccaaanttgn ttgggggaat ttttaaattc ccaannnccc   2040
aaggggggnca atttagnggn ccccnaatcc cccaaaaant ggttcnnggn tnaaancngc   2100
cnnnnccnaa tttntanggg tttacttngn tttaaaaaac ccncccaaaa actcccccnn   2160
gaaccnaaaa aanaaaagga ngccattttt ngnngnaaac tttttttaann nnccnnttaa   2220
angggttaaa aaannnnnnn tnnncccnaa tttttcaaan aang                      2264
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<210> 106
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 106

```
Ser Thr Ser Thr Gln Ala Pro Ala Ala Ser Pro Thr Gly Val Val Pro
1               5                   10                  15
Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
            20                  25                  30
Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
        35                  40                  45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
    50                  55                  60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65                  70                  75                  80
```

```
Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu
                85                  90                  95
Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg
            100                 105                 110
Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe
        115                 120                 125
Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala
    130                 135                 140
Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu
145                 150                 155                 160
Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn
                165                 170                 175
Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn
            180                 185                 190
Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala
        195                 200                 205
Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn
    210                 215                 220
Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln
225                 230                 235                 240
Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu
                245                 250                 255
Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala
            260                 265                 270
Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg
        275                 280                 285
Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys
    290                 295                 300
Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met
305                 310                 315                 320
Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr
                325                 330                 335
Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala
            340                 345                 350
Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala
        355                 360                 365
Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu
    370                 375                 380
```

<210> 107
<211> 1367
<212> DNA
<213> Homo Sapiens

<400> 107

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gcgacacagg cctcgaggct gtctctgaca agtgttcaca ggaggtgggg acgcctctgc      60
gcgaggaacg aggagctacg ggcctgggcc cggttattgc catgggcagc ggctgccgca     120
tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg     180
tccctgaaga cttcatctcc cgagagctgt ttgacacagt ccaagtgtac atcatcacca     240
agccagagct gcagaacaag cttatcactg tcacagctat ggaaaagaag ctgatcggct     300
gtcctgtgtg catcgaacac aagaagtaca gccgcaatgc tctcctcttc aacctgggct     360
tcgtgtgtga tgcccaggcc aagacctgcg ccctcgagcc cattgttaaa aagctggctg     420
gctatctgac cacactagag ctagagagca gcttcgtgtc catggaggag agcaagcaga     480
agttggtgcc catcatgacc atcttgctgg aggagctaaa tgcctcaggc cggtgcactc     540
tgcccattga tgagtccaac accatccact tgaaggtgat tgagcagcgg ccagaccctc     600
```

```
cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact      660
cacagtggga cctcactaca caacaaatcc tgccctacat tgatgggttc cgccacatcc      720
agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattgct atccagaacc      780
tgctgtacta cggcgttgtg acactggtgt ccatcctcca gtactccaat gtatactgcc      840
caacgcccaa ggtccaggac ctggtagatg acaagtccct gcaagaggca tgtctatcct      900
acgtgaccaa gcaagggcac aagagggcca gtctccggga tgtgttccag ctatactgca      960
gcctgagccc tggcactacc gtgcgagacc tcattggccg ccaccccccag cagctgcagc     1020
atgttgatga acggaagctg atccagttcg ggcttatgaa gaacctcatc aggcgactac     1080
agaagtatcc tgtgcgggtg actcgggaag agcagagcca ccctgcccgg ctttatacag     1140
gctgccacag ctatgacgag atctgctgca agacaggcat gagctaccat gagctggatg     1200
agcggcttga aaatgacccc aacatcatca tctgctggaa gtgaggctgg tagtgactgg     1260
atggacacat tgctgtgggt agtccctcct actaggaggc ttgtcatact gtctagaggt     1320
tgactcttag ttctgtaaat aaagacatcc atttcaaaca gccaaaa                  1367
```

```
<210> 108
<211> 413
<212> PRT
<213> Homo Sapiens

<400> 108
Asp Thr Gly Leu Glu Ala Val Ser Asp Lys Cys Ser Gln Glu Val Gly
1               5                   10                  15
Thr Pro Leu Arg Glu Glu Arg Gly Ala Thr Gly Leu Gly Pro Val Ile
            20                  25                  30
Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
        35                  40                  45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
    50                  55                  60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
65                  70                  75                  80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
                85                  90                  95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
            100                 105                 110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
        115                 120                 125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
    130                 135                 140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
145                 150                 155                 160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
                165                 170                 175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
            180                 185                 190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
        195                 200                 205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
    210                 215                 220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
225                 230                 235                 240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
                245                 250                 255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
            260                 265                 270
Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val
```

```
        275                 280                 285
Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln
    290                 295                 300
Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser
305                 310                 315                 320
Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln
                325                 330                 335
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met
            340                 345                 350
Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg
        355                 360                 365
Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr
    370                 375                 380
Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu
385                 390                 395                 400
Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys
                405                 410
```

<210> 109
<211> 2113
<212> DNA
<213> Homo Sapiens

<400> 109

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gtgcggttgg gaacgcggag cggacggatt cgattcaacg gggttccgga ccgcgctgcg     60
ctatggagca ggtcaatgag ctgaaggaga aaggcaacaa ggccctgagc gtgggtaaca    120
tcgatgatgc cttacagtgc tactccgaag ctattaagct ggatccccac aaccacgtgc    180
tgtacagcaa ccgttctgct gcctatgcca agaaaggaga ctaccagaag gcttatgagg    240
atggctgcaa gactgtcgac ctaaagcctg actggggcaa gggctattca cgaaaagcag    300
cagctctaga gttcttaaac cgctttgaag aagccaagcg aacctatgag gagggcttaa    360
aacacgaggc aaataaccct caactgaaag agggtttaca gaatatggag gccaggttgg    420
cagagagaaa attcatgaac cctttcaaca tgcctaatct gtatcagaag ttggagagtg    480
atcccaggac aaggacacta ctcagtgatc ctacctaccg ggagctgata gagcagctac    540
gaaacaagcc ttctgacctg ggcacgaaac tacaagatcc ccggatcatg accactctca    600
gcgtcctcct tggggtcgat ctgggcagta tggatgagga ggaagagatt gcaacacctc    660
caccaccacc ccctcccaaa aaggagacca agccagagcc aatggaagaa gatcttccag    720
agaataagaa gcaggcactg aaagaaaaag agctggggaa cgatgcctac aagaagaaag    780
actttgacac agccttgaag cattacgaca aagccaagga gctggacccc actaacatga    840
cttacattac caatcaagca gcggtatact ttgaaaaggg cgactacaat aagtgccggg    900
agctttgtga gaaggccatt gaagtgggga gagaaaaccg agaagactat cgacagattg    960
ccaaagcata tgctcgaatt ggcaactcct acttcaaaga agaaaagtac aaggatgcca   1020
tccatttcta taacaagtct ctggcagagc accgaacccc agatgtgctc aagaaatgcc   1080
agcaggcaga gaaaatcctg aaggagcaag agcggctggc ctacataaac cccgacctgg   1140
ctttggagga gaagaacaaa ggcaacgagt gttttcagaa aggggactat ccccaggcca   1200
tgaagcatta tacagaagcc atcaaaagga acccgaaaga tgccaaatta tacagcaatc   1260
gagctgcctg ctacaccaaa ctcctggagt tccagctggc actcaaggac tgtgaggaat   1320
gtatccagct ggagccgacc ttcatcaagg gttatacacg gaaagccgct gcgctggaag   1380
cgatgaagga ctacaccaaa gccatggatg tgtaccagaa ggcgctagac ctggactcca   1440
gctgtaagga ggcggcagac ggctaccagc gctgtatgat ggcgcagtac aaccggcacg   1500
acagccccga agatgtgaag cgacgagcca tggccgaccc tgaggtgcag cagatcatga   1560
gtgacccagc catgcgcctt atcctggaac agatgcagaa ggacccccag gcactcagcg   1620
aacacttaaa gaatcctgta atagcacaga agatccagaa gctgatggat gtgggtctga   1680
ttgcaattcg gtgatgactt gttcatcccc ccttcccttc gccctcatgt ggaaagagga   1740
gctgggaccg cggcgagcag cacggagcgg aagggagagc aggggagaga aggcctcatc   1800
tctctatatt tatacataac cccggggaag acacagagac tcgtacctgc gctgtttgtg   1860
```

```
ccgccgctgc ctctgggccc tcccagcaca cgcatggtct cttcaccgct gccctcgagt     1920
tccatgtctc tttcccctgc ccctagttgc tgtctcggct gctctcccat agttggtttt     1980
ttttttattt ggggcagtgg gcatgttatg gggaggggag ggggttcttc cagcctcagg     2040
tcccagctgt ctcacgttgt ttattctgcg tccccttctc caataaaaca agccagttgg     2100
gcgtggttat aac                                                        2113
```

<210> 110
<211> 543
<212> PRT
<213> Homo Sapiens

<400> 110

```
Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser
1               5                   10                  15
Val Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys
            20                  25                  30
Leu Asp Pro His Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr
        35                  40                  45
Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
    50                  55                  60
Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala
65                  70                  75                  80
Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
                85                  90                  95
Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
            100                 105                 110
Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
        115                 120                 125
Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
    130                 135                 140
Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
145                 150                 155                 160
Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
                165                 170                 175
Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
            180                 185                 190
Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Pro Lys Lys Glu
        195                 200                 205
Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
    210                 215                 220
Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
225                 230                 235                 240
Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
                245                 250                 255
Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
            260                 265                 270
Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
        275                 280                 285
Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
    290                 295                 300
Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
305                 310                 315                 320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
                325                 330                 335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu
```

340 345 350
Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn
355 360 365
Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr
370 375 380
Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg
385 390 395 400
Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp
405 410 415
Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr
420 425 430
Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met
435 440 445
Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala
450 455 460
Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp
465 470 475 480
Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln
485 490 495
Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln
500 505 510
Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala
515 520 525
Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
530 535 540

<210> 111
<211> 2765
<212> DNA
<213> Homo Sapiens

<400> 111
gggctgcgac tgacaagcgg ctctgcccgg gaccttctcg ctttcatcta gcgctgcact 60
caatggaggg gcgggcaccg cagtgcttaa tgctgtctta actagtgtag gaaaacggct 120
caacccaccg ctgccgaaat gaagtataag aatcttatgg caagggcctt atatgacaat 180
gtcccagagt gtgccgagga actggccttt cgcaagggag acatcctgac cgtcatagag 240
cagaacacag gggactggga aggatggtgg ctgtgctcgt tacacggtcg gcaaggcatt 300
gtcccaggca accgggtgaa gcttctgatt ggtcccatgc aggagactgc ctccagtcac 360
gagcagcctg cctctggact gatgcagcag acctttggcc aacagaagct ctatcaagtg 420
ccaaacccac aggctgctcc ccgagacacc atctaccaag tgccaccttc ctaccaaaat 480
cagggaattt accaagtccc cactggccac ggcacccaag aacaagaggt atatcaggtg 540
ccaccatcag tgcagagaag cattggggga accagtgggc cccacgtggg taaaaaggtg 600
ataacccccg tgaggacagg ccatggctac gtatacgagt acccatccag ataccaaaag 660
gatgtctatg atatccctcc ttctcatacc actcaagggg tatacgacat ccctccctca 720
tcagcaaaag gccctgtgtt ttcagttcca gtgggagaga taaaacctca aggggtgtat 780
gacatcccgc ctacaaaagg ggtatatgcc attccgccct ctgcttgccg ggatgaagca 840
gggcttaggg aaaaagacta tgacttcccc cctcccatga gacaagctgg aaggccggac 900
ctcagaccgg aggggtttta tgacattcct ccaacctgca ccaagccagc agggaaggac 960
cttcatgtaa aatacaactg tgacattcca ggagctgcag aaccggtggc tcgaaggcac 1020
cagagcctgt ccccgaatca cccacccccg caactcggac agtcagtggg ctctcagaac 1080
gacgcatatg atgtcccccg aggcgttcag tttcttgagc caccagcaga aaccagtgag 1140
aaagcaaacc cccaggaaag ggatggtgtt tatgatgtcc ctctgcataa cccgccagat 1200
gctaaaggct ctcgggactt ggtggatggg atcaaccgat tgtctttctc cagtacaggc 1260
agcacccgga gtaacatgtc cacgtcttcc acctcctcca aggagtcctc actgtcagcc 1320
tccccagctc aggacaaaag gctcttcctg gatccagaca cagctattga gagacttcag 1380

cggctccagc aggcccttga gatgggtgtc tccagcctaa tggcactggt cactaccgac 1440
tggcggtgtt acggatatat ggaaagacac atcaatgaaa tacgcacagc agtggacaag 1500
gtggagctgt tcctgaagga gtacctccac tttgtcaagg gagctgttgc aaatgctgcc 1560
tgcctcccgg aactcatcct ccacaacaag atgaagcggg agctgcaacg agtcgaagac 1620
tcccaccaga tcctgagtca aaccagccat gacttaaatg agtgcagctg gtccctgaat 1680
atcttggcca tcaacaagcc ccagaacaag tgtgacgatc tggaccggtt tgtgatggtg 1740
gcaaagacgg tgcccgatga cgccaagcag ctcaccacaa ccatcaacac caacgcagag 1800
gccctcttca gacccggccc tggcagcttg catctgaaga atgggccgga gagcatcatg 1860
aactcaacgg agtacccaca cggtggctcc cagggacagc tgctgcatcc tggtgaccac 1920
aaggcccagg cccacaacaa ggcactgccc ccaggcctga gcaaggagca ggcccctgac 1980
tgtagcagca gtgatggttc tgagaggagc tggatggatg actacgatta cgtccaccta 2040
cagggtaagg aggagtttga gaggcaacag aaagagctat tggaaaaaga gaatatcatg 2100
aaacagaaca agatgcagct ggaacatcat cagctgagcc agttccagct gttggaacaa 2160
gagattacaa agcccgtgga gaatgacatc tcgaagtgga agccctctca gagcctaccc 2220
accacaaaca gtggcgtgag tgctcaggat cggcagttgc tgtgcttcta ctatgaccaa 2280
tgtgagaccc atttcatttc ccttctcaac gccattgacg cactcttcag ttgtgtcagc 2340
tcagcccagc ccccgcgaat cttcgtggca cacagcaagt ttgtcatcct cagtgcacac 2400
aaactggtgt tcattggaga cacgctgaca cggcaggtga ctgcccagga cattcgcaac 2460
aaagtcatga actccagcaa ccagctctgc gagcagctca agactatagt catggcaacc 2520
aagatggccg ccctccatta ccccagcacc acggccctgc aggaaatggt gcaccaagtg 2580
acagaccttt ctagaaatgc ccagctgttc aagcgctctt tgctggagat ggcaacgttc 2640
tgagaagaaa aaaaagagga aggggactgc gttaacggtt actaaggaaa actggaaata 2700
ctgtctggtt tttgtaaatg ttatctattt ttgtagatat tttatataaa aatgaaatat 2760
tttcc 2765

<210> 112
<211> 834
<212> PRT
<213> Homo Sapiens

<400> 112
Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro
1 5 10 15
Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val
20 25 30
Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu
35 40 45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
50 55 60
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
65 70 75 80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
85 90 95
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
100 105 110
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
115 120 125
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly
130 135 140
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
145 150 155 160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
165 170 175
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
180 185 190

Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile
195 200 205
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala
210 215 220
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp
225 230 235 240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg
245 250 255
Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly
260 265 270
Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
275 280 285
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
290 295 300
Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
305 310 315 320
Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
325 330 335
Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro
340 345 350
Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
355 360 365
Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser
370 375 380
Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys
385 390 395 400
Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu
405 410 415
Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr
420 425 430
Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile
435 440 445
Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His
450 455 460
Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile
465 470 475 480
Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His
485 490 495
Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser
500 505 510
Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu
515 520 525
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln
530 535 540
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly
545 550 555 560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser
565 570 575
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly
580 585 590
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser
595 600 605
Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
610 615 620
Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

625 630 635 640
Glu Arg Gln Gln Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln
645 650 655
Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu
660 665 670
Glu Gln Glu Ile Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys
675 680 685
Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp
690 695 700
Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile
705 710 715 720
Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala
725 730 735
Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser
740 745 750
Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr
755 760 765
Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys
770 775 780
Glu Gln Leu Lys Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His
785 790 795 800
Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp
805 810 815
Leu Ser Arg Asn Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala
820 825 830
Thr Phe

<210> 113
<211> 3429
<212> DNA
<213> Homo Sapiens

<400> 113
gagacaaagc agcgcccgtc tgcttcgggc ctctggaatt tagcgctcgc ccagctagcc 60
gcagaaatga ctgctgtcca tgcaggcaac ataaacttca agtgggatcc taaaagtcta 120
gagatcagga ctctggcagt tgagagactg ttggagcctc ttgttacaca ggttacaacc 180
cttgtaaaca ccaatagtaa agggccctct aataagaaga gaggtcgttc taagaaggcc 240
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gccctaaaac ctgaagtgga taagctgaac attatggcag ccaaaagaca acaggaattg 660
aaagatgttg gccatcgtga tcagatggct gcagctagag gaatcctgca gaagaacgtt 720
ccgatcctct atactgcatc ccaggcatgc ctacagcacc ctgatgtcgc agcctataag 780
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gctgtccgcc aggccctgca ggacctgctt tcggagtaca tgggcaatgc tggacgtaaa 1140
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cgtagacagc tccgcaaagc tgtcatggac cacgtttcag attctttcct ggaaaccaat 1260

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gttccacttt tggtattgat tgaagctgca aagaatggaa atgagaaaga agttaaggag    1320
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tccatctcaa ataatgaaga aggtgtaaag cttgttcgaa tgtctgcaag ccagttagaa    1440
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acagatgctg tcgatgacat tacttccatt gatgacttct tggctgtctc agagaatcac    1620
attttggaag atgtgaacaa atgtgtcatt gctctccaag agaaggatgt ggatggcctg    1680
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gagatggaca actatgagcc aggagtctac acagagaagg ttctggaagc cactaagctg    1800
ctctccaaca cagtcatgcc acgttttact gagcaagtag aagcagccgt ggaagccctc    1860
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tatgatggca tccgggacat caggaaagca gtgctgatga taaggacccc tgaggagttg    1980
gatgactctg actttgagac agaagatttt gatgtcagaa gcaggacgag cgtccagaca    2040
gaagacgatc agctgatagc tggccagagt gcccgggcga tcatggctca gcttccccag    2100
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ttaaatgacc aaagatgacc tgtggtaagc aacctgggca tcttagaagc agtccctgga    3240
gaaggcatgt tcccagaaag gtctctggag ggacaaactc actcagtaaa acataatgta    3300
tcatcatgaa gaaaactgat tctctatgac atgaaatgaa aattttaatg cattgttata    3360
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cgatgccat                                                            3429
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<210> 114
<211> 906
<212> PRT
<213> Homo Sapiens

<400> 114

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Met Thr Ala Val His Ala Gly Asn Ile Asn Phe Lys Trp Asp Pro Lys
1               5                   10                  15
Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
            20                  25                  30
Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
        35                  40                  45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
    50                  55                  60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65                  70                  75                  80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp
```

```
                85                  90                  95
Val Arg Lys Gln Gly Asp Leu Met Lys Ala Ala Ala Gly Glu Phe Ala
            100                 105                 110
Asp Asp Pro Cys Ser Ser Val Lys Arg Gly Asn Met Val Arg Ala Ala
        115                 120                 125
Arg Ala Leu Leu Ser Ala Val Thr Arg Leu Leu Ile Leu Ala Asp Met
    130                 135                 140
Ala Asp Val Tyr Lys Leu Leu Val Gln Leu Lys Val Val Glu Asp Gly
145                 150                 155                 160
Ile Leu Lys Leu Arg Asn Ala Gly Asn Glu Gln Asp Leu Gly Ile Gln
                165                 170                 175
Tyr Lys Ala Leu Lys Pro Glu Val Asp Lys Leu Asn Ile Met Ala Ala
            180                 185                 190
Lys Arg Gln Gln Glu Leu Lys Asp Val Gly His Arg Asp Gln Met Ala
        195                 200                 205
Ala Ala Arg Gly Ile Leu Gln Lys Asn Val Pro Ile Leu Tyr Thr Ala
    210                 215                 220
Ser Gln Ala Cys Leu Gln His Pro Asp Val Ala Ala Tyr Lys Ala Asn
225                 230                 235                 240
Arg Asp Leu Ile Tyr Lys Gln Leu Gln Gln Ala Val Thr Gly Ile Ser
                245                 250                 255
Asn Ala Ala Gln Ala Thr Ala Ser Asp Asp Ala Ser Gln His Gln Gly
            260                 265                 270
Gly Gly Gly Gly Glu Leu Ala Tyr Ala Leu Asn Asn Phe Asp Lys Gln
        275                 280                 285
Ile Ile Val Asp Pro Leu Ser Phe Ser Glu Glu Arg Phe Arg Pro Ser
    290                 295                 300
Leu Glu Glu Arg Leu Glu Ser Ile Ile Ser Gly Ala Ala Leu Met Ala
305                 310                 315                 320
Asp Ser Ser Cys Thr Arg Asp Asp Arg Arg Glu Arg Ile Val Ala Glu
                325                 330                 335
Cys Asn Ala Val Arg Gln Ala Leu Gln Asp Leu Leu Ser Glu Tyr Met
            340                 345                 350
Gly Asn Ala Gly Arg Lys Glu Arg Ser Asp Ala Leu Asn Ser Ala Ile
        355                 360                 365
Asp Lys Met Thr Lys Lys Thr Arg Asp Leu Arg Arg Gln Leu Arg Lys
    370                 375                 380
Ala Val Met Asp His Val Ser Asp Ser Phe Leu Glu Thr Asn Val Pro
385                 390                 395                 400
Leu Leu Val Leu Ile Glu Ala Ala Lys Asn Gly Asn Glu Lys Glu Val
                405                 410                 415
Lys Glu Tyr Ala Gln Val Phe Arg Glu His Ala Asn Lys Leu Ile Glu
            420                 425                 430
Val Ala Asn Leu Ala Cys Ser Ile Ser Asn Asn Glu Glu Gly Val Lys
        435                 440                 445
Leu Val Arg Met Ser Ala Ser Gln Leu Glu Ala Leu Cys Pro Gln Val
    450                 455                 460
Ile Asn Ala Ala Leu Ala Leu Ala Ala Lys Pro Gln Ser Lys Leu Ala
465                 470                 475                 480
Gln Glu Asn Met Asp Leu Phe Lys Glu Gln Trp Glu Lys Gln Val Arg
                485                 490                 495
Val Leu Thr Asp Ala Val Asp Asp Ile Thr Ser Ile Asp Asp Phe Leu
            500                 505                 510
Ala Val Ser Glu Asn His Ile Leu Glu Asp Val Asn Lys Cys Val Ile
        515                 520                 525
```

```
Ala Leu Gln Glu Lys Asp Val Asp Gly Leu Asp Arg Thr Ala Gly Ala
    530                 535                 540
Ile Arg Gly Arg Ala Ala Arg Val Ile His Val Val Thr Ser Glu Met
545                 550                 555                 560
Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr
                565                 570                 575
Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu
            580                 585                 590
Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu
        595                 600                 605
Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp
    610                 615                 620
Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp
625                 630                 635                 640
Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val
                645                 650                 655
Gln Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile
            660                 665                 670
Met Ala Gln Leu Pro Gln Glu Gln Lys Ala Lys Ile Ala Glu Gln Val
        675                 680                 685
Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys
    690                 695                 700
Trp Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys
705                 710                 715                 720
Met Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu
                725                 730                 735
Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala
            740                 745                 750
Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
        755                 760                 765
Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
    770                 775                 780
Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
785                 790                 795                 800
Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
                805                 810                 815
Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
            820                 825                 830
Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
        835                 840                 845
Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
    850                 855                 860
Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
865                 870                 875                 880
Lys Ile Lys Arg Ala Ser Gln Lys Lys His Val Asn Pro Val Gln Ala
                885                 890                 895
Leu Ser Glu Phe Lys Ala Met Asp Ser Ile
            900                 905
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<210> 115
<211> 1701
<212> DNA
<213> Homo Sapiens

<400> 115

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cggccggccg ccatggctaa cgtggctgac acgaagctgt acgacatcct gggcgttccc      60
gcgggcgcca gcgagaacga gctgaagaag gcatacagaa agttagccaa ggaatatcat     120
cctgataaga atccccaaat gcaggagaca aactttaaag aaataagttt tgcatatgaa     180
gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg     240
gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcaccgt tttttgtggg     300
ggattgttcg gcttcatggg caatcagagt agaagtcgaa atggcagaag aagaggagag     360
gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaaccaaa     420
ctacaactta gcaagaatgt gctctgtagt gcatgcagtg gccaaggcgg aaagtctgga     480
gctgtccaaa agtgtagtgc ttgtcgaggt cgaggtgtgc gcatcatgat cagacagctg     540
gctccaggga tggtacaaca gatgcagtct gtgtgctctg attgtaatgg tgaaggagag     600
gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc     660
aagattcttg aagtccacgt agacaaaggc atgaaacatg gacagagaat tacattcact     720
ggggaagcag accaggcccc agagtggaac ccggagacat tgttcttttt gctaccagga     780
gaaaagaaca tggaggtatt tcagagagat gggaatgatt tgcacatgac atataaaata     840
ggacttgttg aagctctatg tggatttcag ttcacattaa gccaccttga tggacgtcag     900
attgtggtga aatacccccc tggcaaagta attgaaccag ggtgtgttcg tgtagttcga     960
ggtgaaggga tgccgcagta tcgtaatccc tttgaaaaag gtgggcttta cataaagttt    1020
gatgtgcagt ttcctgaaaa caactggatc aacccagaca agctttctga actagaagat    1080
cttctgccat ctagaccgga agttcctaac ataattggag aaacagagga ggtagagctt    1140
caggaatttg atagcactcg aggctcagga ggtggtcaga ggcgtgaagc ctataatgat    1200
agctctgatg aagaaagcag cagccatcat ggacctggag tgcagtgtgc ccatcagtaa    1260
actctgcaaa caaattgcac aggtggattt tctttccaca tttgcctgat ttgttctcag    1320
caatccagct ggagtgtctt atcaatccag atgaactgag ggacatctgt tggtctatgt    1380
ataactttta aaattggtat agtatctaca gagtgtataa tttaaactaa ccacaaagct    1440
ttacatcttc attttgactg ttccatagca gaataaagca cttgaaagga aacaagactc    1500
cctttcacac atggattatt ataagtttca atcctggtat ctgtgcttga tttttatcag    1560
ttttgtgtag atttttatgt ttcatatttt aaatttaaat cccacattgt aaagtttgta    1620
caatttgtcc tgaagctttg tgtttggctg cacctgcata agctgctaca aatagaataa    1680
agaatttcat agcctgtaaa a                                              1701
```

<210> 116
<211> 415
<212> PRT
<213> Homo Sapiens

<400> 116

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Met Ala Asn Val Ala Asp Thr Lys Leu Tyr Asp Ile Leu Gly Val Pro
1               5                   10                  15
Ala Gly Ala Ser Glu Asn Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala
            20                  25                  30
Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
        35                  40                  45
Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
    50                  55                  60
Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
65                  70                  75                  80
Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
                85                  90                  95
Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
            100                 105                 110
Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
        115                 120                 125
Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
    130                 135                 140
Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys
```

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145                 150                 155                 160
Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu
                165                 170                 175
Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn
            180                 185                 190
Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu
        195                 200                 205
Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp
    210                 215                 220
Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp
225                 230                 235                 240
Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly
                245                 250                 255
Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met
            260                 265                 270
Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr
        275                 280                 285
Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly
    290                 295                 300
Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met
305                 310                 315                 320
Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe
                325                 330                 335
Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser
            340                 345                 350
Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile
        355                 360                 365
Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly
    370                 375                 380
Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu
385                 390                 395                 400
Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln
                405                 410                 415
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<210> 117
<211> 1821
<212> DNA
<213> Homo Sapiens

<400> 117

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aaacatacaa gcttgcaagg agcttgccca aaccactcgt acagcatatg gaccaaaagg     180
aatgaacaaa atggttatca accacttgga gaagttgttt gtgacaaacg atgcagcaac     240
tattttaaga gaactagaag tacagcatcc tgctgcaaaa atgattgtaa tggcttctca     300
tatgcaagag caagaagttg gagatggcac aaactttgtt ctggtatttg ctggagctct     360
cctggaatta gctgaagaac ttctgaggat tggcctgtca gtttcagagg tcatagaagg     420
ttatgaaata gcctgcagaa aagctcatga gattcttcct aatttggtat gttgttctgc     480
aaaaaacctt cgagatattg atgaagtctc atctctactt cgtacctcca taatgagtaa     540
acaatatggt aatgaagtat ttctggccaa gcttattgct caggcatgcg tatctatttt     600
tcctgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg     660
tatcagttcc tcttcagtat tgcatggcat ggtttttaag aaggaaaccg aaggtgatgt     720
aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac     780
agaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg     840
agaagaaaac ctcatggatg cacaagtcaa agctattgct gatactggtg caaatgtcgt     900
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agtaacaggt ggcaaagtgg cagacatggc tcttcattat gcaaataaat ataatatcat 960
gttagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac 1020
agctcttcct agattgacac ctcctgtcct tgaagaaatg ggacactgtg acagtgttta 1080
cctctcagaa gttggagata ctcaggtggt ggtttttaag catgaaaagg aagatggcgc 1140
catttctacc atagtacttc gaggctctac agacaatctg atggatgaca tagaaagggt 1200
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tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg 1620
tgggcccaag cctccaagtg ggaagaaaga ctgggatgat gaccaaaatg attgaaattg 1680
gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg 1740
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aataaacata ttgttactgt c 1821

<210> 118
<211> 548
<212> PRT
<213> Homo Sapiens

<400> 118
Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
1 5 10 15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
20 25 30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
35 40 45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
50 55 60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65 70 75 80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
85 90 95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100 105 110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115 120 125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
130 135 140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
145 150 155 160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
165 170 175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
180 185 190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
195 200 205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
210 215 220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
225 230 235 240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
245 250 255

Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu
260 265 270
Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala
275 280 285
Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr
290 295 300
Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp
305 310 315 320
Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu
325 330 335
Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu
340 345 350
Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu
355 360 365
Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu
370 375 380
Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys
385 390 395 400
Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu
405 410 415
Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly
420 425 430
Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile
435 440 445
Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile
450 455 460
Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu
465 470 475 480
Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly
485 490 495
Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr
500 505 510
Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys
515 520 525
Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp
530 535 540
Asp Gln Asn Asp
545

<210> 119
<211> 1321
<212> DNA
<213> Homo Sapiens

<400> 119
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ctggtagaca gttactggac gaagtagaag tggcgactga acccgccggt tcccggatag 120
tccaggagaa ggtgttcaag ggcttggacc tccttgagaa ggctgccgaa atgttatcgc 180
agctcgactt gttcagccga aatgaagatt tggaagagat tgcttccacc gacctgaagt 240
acctttggt gccagcgttt caaggagccc tcaccatgaa acaagtcaac cccagcaagc 300
gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt 360
gctatcatgt ggcagagttt gagctgccca aaaccatgaa caactctgct gaaaatcaca 420
ctgccaattc ctccatggct tatcctagtc tcgttgctat ggcatctcaa agacaggcta 480
aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg 540
ctgtggaaag tggtcaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc 600

agaggtggat tgatatcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc 660
tgagagaaag agactcttca agagaggcat caacttctaa ctcatctcgc caggagaggc 720
ctccagtgaa acccttcatt ctcactcgga acatggctca agccaaagta tttggagctg 780
gttatccaag tctgccaact atgacggtga gtgactggta tgagcaacat cggaaatatg 840
gagcattacc ggatcaggga atagccaagg cagcaccaga ggaattcaga aaagcagctc 900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag 960
cccgggagtg ggatgactgg aaggacaccc atcctagggg ctatgggaac cgacagaaca 1020
tgggctgatc ttcccacaac accacaggac tgcagggtgc acaactccct gccaaggaaa 1080
accatgcagt cctcccctcc ctggtctcct gcttcagctc tgtacaacga gggcaaagat 1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta 1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc 1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt 1320
c 1321

<210> 120
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 120
Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
1 5 10 15
Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
20 25 30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
35 40 45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
50 55 60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65 70 75 80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
85 90 95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
100 105 110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
115 120 125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
130 135 140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145 150 155 160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
165 170 175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
180 185 190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
195 200 205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
210 215 220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225 230 235 240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
245 250 255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
260 265 270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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        275                 280                 285
Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu
    290                 295                 300
Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu
305                 310                 315                 320
Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln
                325                 330                 335
Asn Met Gly
```

```
<210> 121
<211> 2965
<212> DNA
<213> Homo Sapiens

<400> 121
gcggaggtcg gcggtcgggt ccgtctctgc ccgcggctgt ggcggcgccg gcggatccag      60
ccttagcgtt cctctctggg cggcggcggc ggcggctcgg ttgacgcctc ctccgccagc     120
tgagcccgcg ggagcccagg acgccgcttc cccgcccatc cccgctcccc gaggccggcc     180
gcctggtcat ggcgcagccg ggcccggctt cccagcctga cgtttctctt cagcaacggg     240
tagcagaatt ggaaaaaatt aatgcagaat ttttacgtgc acaacagcag cttgaacaag     300
aatttaatca aaagagagca aaatttaagg agttatattt ggctaaagag gaggatctga     360
agaggcaaaa tgcagtatta caagctgcac aagatgattt gggacacctt cgaacccagc     420
tgtgggaagc tcaagcagag atggagaata ttaaggcgat tgccacagtc tctgagaaca     480
ccaagcaaga agctatagat gaagtgaaaa gacagtggag agaagaagtt gcttcacttc     540
aggctgttat gaaagaaaca gttcgtgact atgagcacca gttccacctt aggctggagc     600
aggagcgaac acagtgggca cagtatagag aatacgcaga gagggaaata gctgatttaa     660
gaagaaggct gtctgaaggt caagaggagg aaaatttaga aaatgaaatg aaaaaggccc     720
aagaggatgc tgagaaactt cggtccgttg tgatgccaat ggaaaaggaa attgcagctt     780
tgaaggataa actgacagag gctgaagaca aaattaaaga gctggaggcc tcaaaggtta     840
aagaactgaa tcattatctg gaagctgaga aatcttgtag gactgatcta gagatgtatg     900
tagctgtttt gaatactcag aaatctgttc tacaggaaga tgctgagaaa ctgcggaaag     960
aattgcatga agtttgccat ctcttggagc aagagcgaca acaacacaac cagttaaaac    1020
atacgtggca gaaggccaat gaccagtttc tggaatctca gcgtttactg atgagagaca    1080
tgcagcgaat ggagattgtg ctaacttcag aacagctccg acaagttgaa gaactgaaga    1140
agaaagatca ggaggatgat gaacaacaaa gactcaataa gagaaaggat cacaaaaaag    1200
cagatgttga ggaagaaata aaaataccag tagtgtgtgc tttaactcaa gaagaatctt    1260
cagcccagtt atcaaatgaa gaggagcatt tagacagcac ccgtggctca gttcattcct    1320
tagatgcagg cttgctgttg ccatctggag atcctttcag taaatcggac aatgacatgt    1380
ttaaagatgg actcaggaga gcacagtcta cagacagctt gggaacctcg ggctcattgc    1440
aatccaaagc tttaggctat aactacaaag caaaatctgc tggaaacctg gacgagtcag    1500
attttggacc actggtagga gcagattcag tgtctgagaa ctttgatact gcatcccttg    1560
ggtcactcca gatgccaagt gggtttatgt taaccaaaga tcaggaaaga gcaatcaagg    1620
cgatgacacc agaacaagaa gagacagcgt ccctcctctc cagcgttacc cagggcatgg    1680
agagtgccta tgtgtcccct agtggttatc gtttagttag tgaaacagaa tggaatctct    1740
tgcagaaaga ggtacataat gctggaaata aacttggtag acgttgtgat atgtgttcca    1800
attacgaaaa acagttacaa ggaattcaga ttcaggaggc tgaaacgaga gaccaggtga    1860
aaaaactaca gctgatgcta aggcaagcta atgaccagtt agagaagaca atgaaagata    1920
agcaggagct ggaagacttc ataaagcaaa gcagcgaaga ttcgagtcac cagatctctg    1980
cactcgtcct aagagcccag gcctccgaga tcttacttga agagttacag caggggcttt    2040
cccaggcaaa gagggatgtt caggaacaga tggcggtgct gatgcagtca cgggaacagg    2100
tttcagaaga gctggtgagg ttacagaaag ataatgacag tctccaggga aagcacagcc    2160
tgcatgtgtc attacagcaa gcagaagact tcatcctccc agacactaca gaggcactgc    2220
gggagttggt attaaaatac cgtgaggaca tcattaatgt gcggacagca gcagaccacg    2280
tagaagaaaa gctgaaggct gagatacttt tcctaaaaga gcagatccaa gcagaacagt    2340
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gtttaaaaga aaatcttgaa gaaactctgc aactagaaat agaaaactgc aaggaggaaa    2400
tagcttctat ttctagccta aaagctgaat tagaaagaat aaaagtggaa aaggacagt     2460
tggagtccac attaagagag aagtctcaac agcttgagag tcttcaggaa ataaagatca    2520
gtttggaaga gcagttaaag aaagagactg ctgctaaggc taccgttgaa cagctaatgt    2580
ttgaagagaa gaacaaagct cagagattac agacagaatt agatgtcagt gagcaagtcc    2640
agagagattt tgtaaagctt tcacagaccc ttcaggtgca gttagagcgg atccggcaag    2700
ctgactcctt ggagagaatc cgggcaattc tgaatgatac taaactgaca gacattaacc    2760
agcttcctga gacatgacac cctcatggca ggattctagc ctgcactttg ggtttttaac    2820
tcatctttag agcaacagta attattattt aactcttaac tgaagaaaga gaagtcacaa    2880
caaaaggaag actggagaaa tgcttacttc tagagggaga agactgtgcg gcacaggaaa    2940
cagcaaacag tggggtgatc tgcag                                          2965
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<210> 122
<211> 862
<212> PRT
<213> Homo Sapiens

<400> 122
Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
1               5                   10                  15
Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
            20                  25                  30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
        35                  40                  45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
    50                  55                  60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
65                  70                  75                  80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
                85                  90                  95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
            100                 105                 110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
        115                 120                 125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
    130                 135                 140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
145                 150                 155                 160
Leu Ser Glu Gly Gln Glu Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
                165                 170                 175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
            180                 185                 190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
        195                 200                 205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
    210                 215                 220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
225                 230                 235                 240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
                245                 250                 255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
            260                 265                 270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
        275                 280                 285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val
```

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    290                 295                 300
Leu Thr Ser Glu Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp
305                 310                 315                 320
Gln Glu Asp Asp Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys
                325                 330                 335
Lys Ala Asp Val Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu
            340                 345                 350
Thr Gln Glu Glu Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu
        355                 360                 365
Asp Ser Thr Arg Gly Ser Val His Ser Leu Asp Ala Gly Leu Leu Leu
    370                 375                 380
Pro Ser Gly Asp Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp
385                 390                 395                 400
Gly Leu Arg Arg Ala Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser
                405                 410                 415
Leu Gln Ser Lys Ala Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly
            420                 425                 430
Asn Leu Asp Glu Ser Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val
        435                 440                 445
Ser Glu Asn Phe Asp Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser
    450                 455                 460
Gly Phe Met Leu Thr Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr
465                 470                 475                 480
Pro Glu Gln Glu Glu Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly
                485                 490                 495
Met Glu Ser Ala Tyr Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu
            500                 505                 510
Thr Glu Trp Asn Leu Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys
        515                 520                 525
Leu Gly Arg Arg Cys Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln
    530                 535                 540
Gly Ile Gln Ile Gln Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu
545                 550                 555                 560
Gln Leu Met Leu Arg Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys
                565                 570                 575
Asp Lys Gln Glu Leu Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser
            580                 585                 590
Ser His Gln Ile Ser Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile
        595                 600                 605
Leu Leu Glu Glu Leu Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val
    610                 615                 620
Gln Glu Gln Met Ala Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu
625                 630                 635                 640
Glu Leu Val Arg Leu Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His
                645                 650                 655
Ser Leu His Val Ser Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp
            660                 665                 670
Thr Thr Glu Ala Leu Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile
        675                 680                 685
Ile Asn Val Arg Thr Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala
    690                 695                 700
Glu Ile Leu Phe Leu Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys
705                 710                 715                 720
Glu Asn Leu Glu Glu Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu
                725                 730                 735
```

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Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys
            740                 745                 750
Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln
        755                 760                 765
Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys
    770                 775                 780
Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu
785                 790                 795                 800
Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln
                805                 810                 815
Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu
            820                 825                 830
Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu
        835                 840                 845
Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr
    850                 855                 860

      <210> 123
      <211> 544
      <212> DNA
      <213> Homo Sapiens

      <400> 123
gggagtggcg tggcgcaggg atggcacaaa agaaatatct tcaagcaaaa ttgacccagt      60
ttttaaggga agacaggatt caactttgga aacctccata tacagatgaa aataaaaaag     120
ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa     180
atgaagtaga aaaggtaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa     240
atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacca ccaagactaa     300
aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt     360
ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga     420
agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga     480
tggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttccag ttagaggaag     540
agga                                                                  544

      <210> 124
      <211> 178
      <212> PRT
      <213> Homo Sapiens

      <400> 124
Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys
 1               5                  10                  15
Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro
            20                  25                  30
Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala
        35                  40                  45
Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys
    50                  55                  60
Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn
65                  70                  75                  80
Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro
                85                  90                  95
Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His
            100                 105                 110
Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu
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        115                 120                 125
Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys
    130                 135                 140
Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu
145                 150                 155                 160
Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu
                165                 170                 175
Glu Glu
```

```
<210> 125
<211> 1302
<212> DNA
<213> Homo Sapiens

<400> 125
atggaggtgg tggaccccgca gcagctgggc atgttcacgg agggcgagct gatgtcggtg      60
ggtatggaca cgttcatcca ccgcatcgac tccaccgagg tcatctacca gccgcgccgc     120
aagcgggcca agctcatcgg caagtacctg atgggggacc tgctgggggga aggctcttac     180
ggcaaggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc     240
aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa     300
ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa     360
gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg     420
gacagcgtgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg     480
attgacggcc tggagtacct gcatagccag ggcattgtgc acaaggacat caagccgggg     540
aacctgctgc tcaccaccgg tggcaccctc aaaatctccg acctgggcgt ggccgaggca     600
ctgcacccgt tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag     660
ccgccccgaga ttgccaacgg cctggacacc ttctccggct tcaaggtgga catctggtcg     720
gctggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc     780
tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcga ctgtggcccc     840
ccgctctctg acctgctgaa agggatgctt gagtacgaac cggccaagag gttctccatc     900
cggcagatcc ggcagcacag ctggttccgg aagaaacatc ctccggctga agcaccagtg     960
cccatcccac cgagcccaga caccaaggac cggtggcgca gcatgactgt ggtgccgtac    1020
ttggaggacc tgcacggcgc ggacgaggac gaggacctct tcgacatcga ggatgacatc    1080
atctacactc aggacttcac ggtgcccgga caggtcccag aagaggaggc cagtcacaat    1140
ggacagcgcc ggggcctccc caaggccgtg tgtatgaacg gcacagaggc ggcgcagctg    1200
agcaccaaat ccagggcgga gggccgggcc cccaaccctg cccgcaaggc ctgctccgcc    1260
agcagcaaga tccgccggct gtcggcctgc aagcagcagt ga                       1302
```

```
<210> 126
<211> 433
<212> PRT
<213> Homo Sapiens

<400> 126
Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu
 1               5                  10                  15
Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr
            20                  25                  30
Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
        35                  40                  45
Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
    50                  55                  60
Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
65                  70                  75                  80
```

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys
85 90 95
Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln
100 105 110
Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val
115 120 125
Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro
130 135 140
Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu
145 150 155 160
Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp
165 170 175
Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile
180 185 190
Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp
195 200 205
Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile
210 215 220
Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
225 230 235 240
Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
245 250 255
Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr
260 265 270
Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly
275 280 285
Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
290 295 300
Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val
305 310 315 320
Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
325 330 335
Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp
340 345 350
Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val
355 360 365
Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg
370 375 380
Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu
385 390 395 400
Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys
405 410 415
Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln
420 425 430
Gln

<210> 127
<211> 1488
<212> DNA
<213> Homo Sapiens

<400> 127
gaggggcggg gcggtgccgg caagatggct gcgcccgaga agatgacgtt tcccgagaaa 60
ccaagccaca aaaagtacag ggccgccctg aagaaggaga aacgaaagaa acgtcggcag 120

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt     180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat     240
gaggagtggt tgctaagaga gcagaaggca caagaagaat tcagaataaa gaaggaaaag     300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaaagga acaatgggaa     360
gaacagcaga ggaaagagag agaagaggag gagcagaaac gacaggagaa gaaagaaaaa     420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tggtaccaca     480
tggcaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt     540
cccttctaca gtaaaacagg agcttgcaga tttggagata gatgttcacg taaacataat     600
ttcccaacat ccagtcctac ccttcttatt aagagcatgt ttacgacgtt tggaatggag     660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc     720
taccaacagt tcctagactt ctatgaggat gtgttgcccg agttcaagaa cgtggggaaa     780
gtgattcagt tcaaggtcag ctgcaatttg gaacctcacc tgaggggcaa tgtatatgtt     840
cagtaccagt cggaagaaga atgccaagca gccctttctc tgtttaacgg acgatggtat     900
gcaggacgac agctgcagtg tgaattctgc cccgtgaccc ggtggaaaat ggcgatttgt     960
ggtttatttg aaatacaaca atgtccaaga ggaaagcact gcaactttct tcatgtgttc    1020
agaaatccca acaatgaatt ctgggaagct aatagagaca tctacttgtc tccagatcgg    1080
actggctcct cctttgggaa gaactccgaa aggagggaga ggatgggcca ccacgacgac    1140
tactacagca ggctgcgggg aaggagaaac cctagtccag accactccta caaaagaaat    1200
ggggaatccg agaggaaaag tagtcgtcac agggggaaga aatctcacaa acgcacatca    1260
aagagtcggg agaggcacaa ttcacgaagc agaggaagaa atagggaccg cagcagggac    1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc    1380
agccggagcc aaagttcctc taggtcccga agtcgtggca ggaggaggtc gggtaataga    1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt                 1488
```

<210> 128
<211> 482
<212> PRT
<213> Homo Sapiens

<400> 128

```
Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
1               5                   10                  15
Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
            20                  25                  30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
        35                  40                  45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu Leu
    50                  55                  60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65                  70                  75                  80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
                85                  90                  95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
            100                 105                 110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln Glu
        115                 120                 125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
    130                 135                 140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145                 150                 155                 160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
                165                 170                 175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
            180                 185                 190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr
```

```
        195                 200                 205
Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser
    210                 215                 220
Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr
225                 230                 235                 240
Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe
                245                 250                 255
Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val
            260                 265                 270
Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn
        275                 280                 285
Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val
    290                 295                 300
Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys
305                 310                 315                 320
Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn
                325                 330                 335
Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg
            340                 345                 350
Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly
        355                 360                 365
His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser
    370                 375                 380
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser
385                 390                 395                 400
Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu
                405                 410                 415
Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp
            420                 425                 430
Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg
        435                 440                 445
Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg
    450                 455                 460
Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys
465                 470                 475                 480
Ser Lys
```

```
<210> 129
<211> 1663
<212> DNA
<213> Homo Sapiens

<400> 129
aggccctgag ccaactccgg gtgctctgct gtgagtggct gaggcccgag atccacacca     60
aggagcagat cctggagcta ctggtgctgg agcagttcct gaccatcctg ccccaggagc    120
tccaggcctg ggtgcaggag cattgcccgg agagcgctga agaggctgtc actctcctcg    180
aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac    240
agaaaccggt gtgggagaag atatcctcct caggaactgc aaaggaatcc ccgagcagca    300
tgcagccaca gcccttggag accagtcaca aatacgagtc ttgggggccc ctgtacatcc    360
aagagtctgg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat    420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca    480
aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt    540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccccctct tcaagaggca ggctccaaga    600
aaggtagaga atcagttcct actaaaccta ccccaggaga gagacgttat atatgtgctg    660
```

aatgtggcaa agcctttagt aatagctcaa atctcaccaa acacaggaga acacacactg 720
gggagaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca 780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt 840
ttgggcagag ctcagacctt cttaaacatc agagaatgca cacagaagag gcgccatatc 900
agtgcaaaga ttgtggcaag gctttcagcg ggaaaggcag cctcattcgt cactatcgga 960
tccacactgg ggagaagcct tatcagtgta acgaatgtgg gaagagcttc agtcagcatg 1020
cgggcctcag ctcccaccag agactccaca ccggagagaa gccatataag tgtaaggagt 1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaatc cacaccgggg 1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca 1200
aacatcagcg agtccacact ggagagggag aagcaccgta actttcaagc gctcctgttg 1260
ttgtcgttgt tttaaacttt agaatctgaa aaccagaaag aagtcttgtc attgcagcag 1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag ggatgcctg aggagtgcga 1380
gctccacagc aacatggcag gcaggaggtc ctcagaaggt gtcaggaggt tccacactcg 1440
ccagttcact ggagcagagt cccttcgcca cacttagggt cccagtaagc catgccagca 1500
ttaccttttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga 1560
ttgtttaatt tttaacatat attcaagaat tttaatttgt aaagaattga gccacattga 1620
acacaattga atgagattca gaataaactt ataacatctt aaa 1663

<210> 130
<211> 412
<212> PRT
<213> Homo Sapiens

<400> 130

Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
1 5 10 15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
20 25 30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
35 40 45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
50 55 60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
65 70 75 80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
85 90 95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
100 105 110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
115 120 125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
130 135 140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
145 150 155 160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
165 170 175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
180 185 190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
195 200 205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
210 215 220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
225 230 235 240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

```
                245                 250                 255
Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr
            260                 265                 270
Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys
        275                 280                 285
His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys
    290                 295                 300
Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile
305                 310                 315                 320
His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe
                325                 330                 335
Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu
            340                 345                 350
Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser
        355                 360                 365
Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp
    370                 375                 380
Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys
385                 390                 395                 400
His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro
                405                 410

<210> 131
<211> 724
<212> DNA
<213> Homo Sapiens

<400> 131
ggagaatgaa aagcagaaag tggcagagct gtattctatc cataactctg gagacaaatc      60
tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc     120
tagtagcttg caggaagatc tggctcatac ccgaaatgat gccaatcgat tacaggatgc     180
cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga     240
agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaag     300
gagtgacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt     360
gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga     420
ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc     480
tgcggaatgg cggcagtttc aggctgatct ccagactgca gtagtcattg caaatgacat     540
taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggctcaaga     600
aaaaaatgag aaactcacaa aagaattgga ggaaataagt ccgccaagcc agaagangac     660
gangccggta ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag     720
ggaa                                                                  724

<210> 132
<211> 218
<212> PRT
<213> Homo Sapiens

<400> 132
Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser
 1               5                  10                  15
Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp
            20                  25                  30
Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala
        35                  40                  45
His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val
```

```
    50                  55                  60
Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu
65                  70                  75                  80
Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys
                85                  90                  95
Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp
            100                 105                 110
Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile
        115                 120                 125
Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp
    130                 135                 140
Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser
145                 150                 155                 160
Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile
                165                 170                 175
Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys
            180                 185                 190
Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu
        195                 200                 205
Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys
    210                 215
```

<210> 133
<211> 719
<212> DNA
<213> Homo Sapiens

<400> 133

```
gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgacgc      60
tggtggaggg tttgcagaaa caacccagga gaccaaggcg gtgactgtcc atgttcacgg     120
ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaatga     180
gctgcaggat cctgtgcaaa gctcgacccc cgagcagtct cctgaggaaa ccacacagag     240
cccagatctg gggcaccgg cagagcagcg tccacaccag gaagaggagc tccagacccct     300
gcaggagagc gaggtcccag tgcccgagga cccagacctt cctgcagaga ggagctctgg     360
agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga     420
tgtggccgta tgcttttccc aggaccagtg gagtgatctg gacccaacac agaaagagtt     480
ctatggagaa tatgtcttgg aagaagactg tggaattgtt gtctctctgt catttccaat     540
ccccagacct gatgagatct cccaggttag agaggaagag cccttgggtc ccagatatcc     600
aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga     660
gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca      719
```

<210> 134
<211> 217
<212> PRT
<213> Homo Sapiens

<400> 134

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Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly
 1               5                  10                  15
Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys
            20                  25                  30
Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr
        35                  40                  45
Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro
    50                  55                  60
```

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser
65 70 75 80
Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu
85 90 95
Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp
100 105 110
Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu
115 120 125
Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys
130 135 140
Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe
145 150 155 160
Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu
165 170 175
Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu
180 185 190
Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg
195 200 205
Asn Pro Glu Phe Tyr Leu His Arg Arg
210 215

<210> 135
<211> 1027
<212> DNA
<213> Homo Sapiens

<400> 135
gcgagggcga gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60
actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg ccactggacg 120
cgcacgtgct ggaaccggat gaggacctgc agcgcctgca gctctcgcgc cagcagctcc 180
aggtcacggg agacgccagc gagagcgccg aggacatctt cttccggcgg gccaaggagg 240
gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300
tgtgggccga caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacgggct 360
tcgagtggaa caagtacaac cagacgcact acgactttga caacccaccg cccaagatcg 420
tgcagggata caagttcaac atcttctacc ccgacctcat cgacaagcgc tccacgcccg 480
agtacttcct ggaggcctgc gccgacaaca aggatttcgc catcctgcgc ttcacgcggg 540
gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtgggaata ctngcaccgc 600
cacggcttcc gctgccagtt tgccaacggc attttccanc tgngctttca cttcaagcgc 660
tnccgctatc ggcggtgacg gccctgggga acggcaggcc aggagggccg agggccacac 720
gggtgccaca gcccaggtcg gagtggccca gccggcaggc ttgtttttca gcatccgacg 780
ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840
acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900
ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttggt 960
ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacgtt gtattttaga 1020
ataaaaa 1027

<210> 136
<211> 299
<212> PRT
<213> Homo Sapiens

<400> 136
Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln
1 5 10 15
Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr

```
                20                      25                      30
Ala His Glu Leu Pro Leu Asp Ala His Val Leu Glu Pro Asp Glu Asp
        35                      40                      45
Leu Gln Arg Leu Gln Leu Ser Arg Gln Gln Leu Gln Val Thr Gly Asp
    50                      55                      60
Ala Ser Glu Ser Ala Glu Asp Ile Phe Phe Arg Arg Ala Lys Glu Gly
65                      70                      75                      80
Met Gly Gln Asp Glu Ala Gln Phe Ser Val Glu Met Pro Leu Thr Gly
                    85                      90                      95
Lys Ala Tyr Leu Trp Ala Asp Lys Tyr Arg Pro Arg Lys Pro Arg Phe
                100                     105                     110
Phe Asn Arg Val His Thr Gly Phe Glu Trp Asn Lys Tyr Asn Gln Thr
        115                     120                     125
His Tyr Asp Phe Asp Asn Pro Pro Pro Lys Ile Val Gln Gly Tyr Lys
    130                     135                     140
Phe Asn Ile Phe Tyr Pro Asp Leu Ile Asp Lys Arg Ser Thr Pro Glu
145                     150                     155                     160
Tyr Phe Leu Glu Ala Cys Ala Asp Asn Lys Asp Phe Ala Ile Leu Arg
                    165                     170                     175
Phe Thr Arg Gly Arg Leu Arg Gly His Arg Phe Gln Asp Arg Gln Pro
                180                     185                     190
Arg Val Gly Ile Leu Ala Pro Pro Arg Leu Pro Leu Pro Val Cys Gln
        195                     200                     205
Arg His Phe Pro Leu Ser Leu Gln Ala Leu Pro Leu Ser Ala Val Thr
    210                     215                     220
Ala Leu Gly Asn Gly Arg Pro Gly Gly Pro Arg Ala Thr Arg Val Pro
225                     230                     235                     240
Gln Pro Arg Ser Glu Trp Pro Ser Arg Gln Ala Cys Phe Ser Ala Ser
                    245                     250                     255
Asp Gly Asn Ile Ser Asn Arg Ser Lys Thr Glu Ser Ala Ser Arg Thr
                260                     265                     270
Pro Arg Gly Pro Pro Asn Leu Thr Ser His Gln Pro Gln Thr Thr His
        275                     280                     285
Ser Pro Ser Gln Thr Pro Arg Leu Ile Trp Lys
    290                     295
```

<210> 137
<211> 766
<212> DNA
<213> Homo Sapiens

<400> 137

```
caaaggttta cacagtaaac aatgtgaatg tgatcaccaa aatacgcaca gaacatctga     60
ccgaggagga aaaaaagaga tataaagaca ggaacccgct ggaatctttg ctgggaactg    120
tggaacacca atttggtgca caaggggacc tcaccacgga atgtgctact gcaaacaacc    180
ccacagccat cacgcctgat gagtacttca atgaagagtt tgatctgaaa gacagggaca    240
ttggaaggcc gaaagagctg acgattagaa cacagaagtt taaagcaatg ttgtggatgt    300
gtgaagagtt tcccctctct ctggtggagc aggtcattcc catcattgac ctaatggctc    360
gaacgagtgc tcattttgca agactgagag atttcatcaa attggaattc ccacctggat    420
ttcctgtcaa aatagcttcc cacatcacaa actttgaggt tgatcaatct gtgtttgaaa    480
ttcccgaatc ttactatgtt caagacaatg gcagaaatgt gcatttgcaa gatgaagatt    540
acgagataat gcagtttgcc atccagcaaa gtctgctgga gtccagcagg agccaggaac    600
tttcaggacc agcttcgaat ggagggatca gccagacaaa cacctatgac gcccagtatg    660
agagggccat ncaggagagc cttctaccag cacagaaagc ctgtgccccc agcgcccctg    720
agcgagacna gccgttttga taatggactt gcagctaagc catgga                   766
```

<210> 138
<211> 243
<212> PRT
<213> Homo Sapiens

<400> 138
Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr
1   5   10   15
Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro
            20   25   30
Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly
        35   40   45
Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr
    50   55   60
Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile
65   70   75   80
Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met
                85   90   95
Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile
            100   105   110
Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu
        115   120   125
Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile
    130   135   140
Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile
145   150   155   160
Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln
                165   170   175
Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu
            180   185   190
Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly
        195   200   205
Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu
    210   215   220
Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg
225   230   235   240
Asp Pro Phe

<210> 139
<211> 3060
<212> DNA
<213> Homo Sapiens

<400> 139
ccgggcggga gtgcggcgag agccggctgg ctgagcttag cgtccgagga ggcggcggcg 60
gcggcggcgg cagcggcggc ggcggggctg tggggcggtg cggaagcgag aggcgaggag 120
cgcgcgggcc gtggccagag tctggcggcg gcctggcgga gcggagagca gcgcccgcgc 180
ctcgccgtgc ggaggagccc cgcacacaat agcggcgcgc gcagcccgcg cccttccccc 240
cggcgcgccc cgccccgcgc gccgagcgcc ccgctccgcc tcacctgcca ccagggagtg 300
ggcgggcatt gttcgccgcc gccgccgccg cgcggggcca tgggggccgc ccggcgcccg 360
gggccgggcc tggcgaggcc gccgcgccgc cgctgagacg ggccccgcgc gcagcccggc 420
ggcgcaggta aggccggccg cgccatggtg gacccggtgg gcttcgcgga ggcgtggaag 480
gcgcagttcc cggactcaga gcccccgcgc atggagctgc gctcagtggg cgacatcgag 540
caggagctgg agcgctgcaa ggcctccatt cggcgcctgg agcaggaggt gaaccaggag 600

cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg 660
cagcgatggg gcttccggcg cgcggcgcag gcccccgacg gcgcctccga gccccgagcg 720
tccgcgtcgc gcccgcagcc agcgcccgcc gacggagccg acccgccgcc cgccgaggag 780
cccgaggccc ggcccgacgg cgagggttct ccgggtaagg ccaggcccgg gaccgcccgc 840
aggcccgggg cagccgcgtc gggggaacgg gacgaccggg gaccccccgc cagcgtggcg 900
gcgctcaggt ccaacttcga gcggatccgc aagggccatg gccagcccgg ggcggacgcc 960
gagaagccct tctacgtgaa cgtcgagttt caccacgagc gcggcctggt gaaggtcaac 1020
gacaaagagg tgtcggaccg catcagctcc ctgggcagcc aggccatgca gatggagcgc 1080
aaaaagtccc agcacggcgc gggctcgagc gtgggggatg catccaggcc cccttaccgg 1140
ggacgctcct cggagagcag ctgcggcgtc gacggcgact acgaggacgc cgagttgaac 1200
ccccgcttcc tgaaggacaa cctgatcgac gccaatggcg gtagcaggcc cccttggccg 1260
cccctggagt accagcccta ccagagcatc tacgtcgggg gcatgatgga aggggagggc 1320
aagggcccgc tcctgcgcag ccagagcacc tctgagcagg agaagcgcct tacctggccc 1380
cgcaggtcct actccccccg gagttttgag gattgcggag gcggctatac ccggactgc 1440
agctccaatg agaacctcac ctccagcgag gaggacttct cctctggcca gtccagccgc 1500
gtgtccccaa gccccaccac ctaccgcatg ttccgggaca aagccgctc tccctcgcag 1560
aactcgcaac agtccttcga cagcagcagt ccccccacgc cgcagtgcca taagcggcac 1620
cggcactgcc cggttgtcgt gtccgaggcc accatcgtgg gcgtccgcaa gaccgggcag 1680
atctggccca acgatggcga gggcgccttc catggagacg cagatggctc gttcggaaca 1740
ccacctggat acggctgcgc tgcagaccgg gcagaggagc agcgccggca ccaagatggg 1800
ctgccctaca ttgatgactc gccctcctca tcgccccacc tcagcagcaa gggcaggggc 1860
agccgggatg cgctggtctc gggagccctg gagtccacta aagcgagtga gctggacttg 1920
gaaaagggct tggagatgag aaaatgggtc ctgtcgggaa tcctggctag cgaggagact 1980
tacctgagcc acctggaggc actgctgctg cccatgaagc ctttgaaagc cgctgccacc 2040
acctctcagc cggtgctgac gagtcagcag atcgagacca tcttcttcaa agtgcctgag 2100
ctctacgaga tccacaagga gttctatgat gggctcttcc cccgcgtgca gcagtggagc 2160
caccagcagc gggtgggcga cctcttccag aagctggcca gccagctggg tgtgtaccgg 2220
gccttcgtgg acaactacgg agttgccatg gaaatggctg agaagtgctg tcaggccaat 2280
gctcagtttg cagaaatctc cgagaacctg agagccagaa gcaacaaaga tgccaaggat 2340
ccaacgacca agaactctct ggaaactctg ctctacaagc ctgtggaccg tgtgacgagg 2400
agcacgctgg tcctccatga cttgctgaag cacactcctg ccagccaccc tgaccacccc 2460
ttgctgcagg acgccctccg catctcacag aacttcctgt ccagcatcaa tgaggagatc 2520
acaccccgac ggcagtccat gacggtgaag aagggagagc accggcagct gctgaaggac 2580
agcttcatgg tggagctggt ggagggggcc cgcaagctgc gccacgtctt cctgttcacc 2640
gagctgcttc tctgcaccaa gctcaagaag cagagcggag gcaaaacgca gcagtatgac 2700
tgcaaatggt acattccgct cacggatctc agcttccaga tggtggatga actggaggca 2760
gtgcccaaca tccccctggt gcccgatgag gagctggacg ctttgaagat caagatctcc 2820
cagatcaaga gtgacatcca gagagagaag agggcgaaca agggcagcaa ggctacggag 2880
aggctgaaga agaagctgtc ggagcaggag tcactgctgc tgcttatgtc tcccagcatg 2940
gccttcaggg tgcacagccg caacggcaag agttacacgt tcctgatctc ctctgactat 3000
gagcgtgcag agtggaggga gaacatccgg gagcagcaga agaagtgttt cagaagcttc 3060

<210> 140
<211> 872
<212> PRT
<213> Homo Sapiens

<400> 140
Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15
Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala

50 55 60
Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80
Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95
Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125
Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130 135 140
Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145 150 155 160
Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165 170 175
Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180 185 190
Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195 200 205
Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210 215 220
Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225 230 235 240
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245 250 255
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260 265 270
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
500 505 510
Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
515 520 525
Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
530 535 540
Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
545 550 555 560
Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
565 570 575
Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
580 585 590
Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
595 600 605
Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
610 615 620
Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
625 630 635 640
Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
645 650 655
Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
660 665 670
Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
675 680 685
Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
690 695 700
Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
705 710 715 720
Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
725 730 735
Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
740 745 750
Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
755 760 765
Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
770 775 780
Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
785 790 795 800
Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
805 810 815
Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
820 825 830
Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
835 840 845
Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
850 855 860
Gln Lys Lys Cys Phe Arg Ser Phe
865 870

<210> 141
<211> 691
<212> DNA
<213> Homo Sapiens

<400> 141

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gacccctcac actcacctag ccaccatgga catcgccatc caccacccct ggatccgccg      60
cccettcttt cctttccact cccccagccg cctctttgac cagttcttcg gagagcacct     120
gttggagtct gatctttttcc cgacgtctac ttccctgagt cccttctacc ttcggccacc    180
ctccttcctg cgggcaccca gctggtttga cactggactc tcagagatgc gcctggagaa     240
ggacaggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaac tcaaagttaa     300
ggtgttggga gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg     360
tttcatctcc agggagttcc acaggaaata ccggatccca gctgatgtag accctctcac     420
cattacttca tccctgtcat ctgatggggt cctcactgtg aatggaccaa ggaaacaggt     480
ctctggccct gagcgcacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcagc     540
cccccaagaaa tagatgccct ttcttgaatt gcatttttta aaacaagaaa gtttccccac    600
cagtgaatga aagtcttgtg actagtgctg aagcttatta atgctaaggg caggcccaaa     660
ttatcaagct aataaaatat cattcagcaa c                                     691
```

<210> 142
<211> 175
<212> PRT
<213> Homo Sapiens

<400> 142

```
Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1               5                   10                  15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
            20                  25                  30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
        35                  40                  45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
    50                  55                  60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65                  70                  75                  80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
                85                  90                  95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
            100                 105                 110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
        115                 120                 125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
    130                 135                 140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145                 150                 155                 160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
                165                 170                 175
```

<210> 143
<211> 1300
<212> DNA
<213> Homo Sapiens

<400> 143

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atctgctggg aatttcttgg gttgacagct cttggatccc tattttgaac agtggtagtg      60
tcctggatta cttttcagaa agaagtaatc ctttttatga cagaacatgt aataatgaag     120
tggtcaaaat gcagaggcta acattagaac acttgaatca gatggttgga atcgagtaca     180
tccttttgca tgctcaagag cccattcttt tcatcattcg gaagcaacag cggcagtccc     240
ctgcccaagt tatcccacta gctgattact atatcattgc tggagtgatc tatcaggcac     300
cagacttggg atcagttata aactctagag tgcttactgc agtgcatggt attcagtcag     360
cttttgatga agctatgtca tactgtcgat atcatccttc caaagggtat tggtggcact     420
```

```
tcaaagatca tgaagagcaa gataaagtca gacctaaagc caaaaggaaa gaagaaccaa    480
gctctatttt tcagagacaa cgtgtggatg ctttactttt agacctcaga caaaaatttc    540
cacccaaatt tgtgcagcta aagcctggag aaaagcctgt tcaagtggat caaacaaaga    600
aagaggcaga acctatacca gaaactgtaa aacctgagga gaaggagacc cccnnagaat    660
gtacaaccag accgggagtg ctaaaggccc ccctgaaaaa cggatgagac ttcagtgagt    720
actggacaaa agagaagcct ggaagactcc tcatgctagt tatcatacct cagtactgtg    780
gctcttgagc tttgaagtac tttattgtaa ccttcttatt tgtatggaat gcgcttattt    840
tttgaaagga tattaggccg gatgtggtgg ctcacgcctg taatcccagc actttgggag    900
gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc aatatggtga    960
aaccccgtct ctactaaaaa tacaaaaatt agccgggcgt ggtggcgggc gcccgtagtc   1020
ccagctactc gggaggctga gacaggagac ttgcttgaac ccgggaggtg gaggttgccc   1080
tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac tttgtctcaa   1140
aaaagaagaa aagatattac tcccatcatg atttcttgtg aatatttgtt atatgtcttc   1200
tgtaaccttt cctctcccgg acttgagcaa cctacacact cacatgttta ctggtagata   1260
tgtttaaaag caaaataaag gtatttgtat atattgaaaa                         1300
```

<210> 144
<211> 233
<212> PRT
<213> Homo Sapiens

<400> 144

```
Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn
 1               5                  10                  15
Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr
            20                  25                  30
Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu
        35                  40                  45
Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala
    50                  55                  60
Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro
65                  70                  75                  80
Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile
                85                  90                  95
Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr
            100                 105                 110
Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys
        115                 120                 125
Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu
    130                 135                 140
Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser
145                 150                 155                 160
Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg
                165                 170                 175
Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys Pro
            180                 185                 190
Val Gln Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu Thr
        195                 200                 205
Val Lys Pro Glu Glu Lys Glu Thr Pro Glu Cys Thr Thr Arg Pro Gly
    210                 215                 220
Val Leu Lys Ala Pro Leu Lys Asn Gly
225                 230
```

<210> 145
<211> 1528

<212> DNA
<213> Homo Sapiens

<400> 145
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ccccccttttt tttttaaact aaaatggagg ctggtttctt gccttaagga gcccattgcc     60
tttcccgctg aagtctagat gttgacatgt aataaagcgg gcagcaggat ggtggtggat    120
gcggccaact ccaatgggcc tttccagccc gtggtccttc tccatattcg agatgttcct    180
cctgctgatc aagagaagct tttatccag aagttacgtc agtgttgcgt cctctttgac     240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt    300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttacccagaa    360
gtagtccata tgtttgcagt taacatgttt cgaacattac caccttcctc caatcctacg    420
ggagcggaat ttgacccgga ggaagatgaa ccaacgttag aagcagcctg gcctcatcta    480
cagcttgttt atgaattttt cttaagattt ttagagtctc cagatttcca acctaatata    540
gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagtgaa    600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta    660
ggcttgagag cttacatcag aaaacagata aataatatat tttataggtt tatttatgaa    720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga    780
tttgccttac cactaaaaga agagcacaag attttcttat tgaaggtgtt actacctttg    840
cacaaagtga aatctctgag tgtctaccat ccccagctgg catactgtgt agtgcagttt    900
ttagaaaagg acagcaccct cacggaacca gtggtgatgg cacttctcaa atactggcca    960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc   1020
attgaaccat cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt   1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac   1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tccttccttg   1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgccctg   1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca   1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa   1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggcccaggg   1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt   1500
tcactaacgt tgtatatgaa aatgtctg                                      1528
```

<210> 146
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 146
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Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
 1               5                   10                  15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
            20                  25                  30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
        35                  40                  45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
    50                  55                  60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
65                  70                  75                  80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
                85                  90                  95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
            100                 105                 110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
        115                 120                 125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Phe Leu Arg Phe
    130                 135                 140
```

```
Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp
145                 150                 155                 160
Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro
                165                 170                 175
Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys
            180                 185                 190
Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe
        195                 200                 205
Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu
    210                 215                 220
Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys
225                 230                 235                 240
Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys
                245                 250                 255
Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val
            260                 265                 270
Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala
        275                 280                 285
Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe
    290                 295                 300
Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe
305                 310                 315                 320
Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser
                325                 330                 335
Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn
            340                 345                 350
Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro
        355                 360                 365
Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys
    370                 375                 380
Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met
385                 390                 395                 400
Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys
                405                 410                 415
Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys
            420                 425                 430
Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile
        435                 440                 445
Thr
```

<210> 147
<211> 1580
<212> DNA
<213> Homo Sapiens

<400> 147

```
atcccctccg gttttcctca gtctccacgt acgtccctca aagcgcgtcc taaaacccgg      60
ataaccggag cgctccccat ggaccacacg gagggcttgc ccgcggagga gccgcctgcg     120
catgctccat cgcctgggaa atttggtgag cggcctccac ctaaacgact tactagggaa     180
gctatgcgaa attatttaaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa     240
gttgcacaga agtcatatgg aaatgaaaaa aggttttttt gcccacctcc ttgtgtatat     300
cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa     360
caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag     420
ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac     480
```

aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt 540
gtgttcctca gcaagcggat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgcctcagga acaaaggtgg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa 780
ttcacagtcc gagatgtcta catccattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat tttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
aaagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat 1080
aaggcagagt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcactccaaa tttacgagtg tggtttgggg atgtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt 1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tggtccgaaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccacg gccacattgc 1440
agtgtagcag gagcaatcct tccagccaat tcaagccagg tgcccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta 1580

<210> 148
<211> 500
<212> PRT
<213> Homo Sapiens

<400> 148
Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
1 5 10 15
Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
20 25 30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
35 40 45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
50 55 60
Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
65 70 75 80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
85 90 95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
100 105 110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
115 120 125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
130 135 140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
145 150 155 160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
165 170 175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
180 185 190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
195 200 205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
210 215 220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

225 230 235 240
Tyr Ile His Tyr Gly Gln Thr Cys Lys Leu Val Cys Ser Val Thr Gly
245 250 255
Met Ala Leu Pro Arg Leu Ile Ile Met Lys Val Asp Lys His Thr Ala
260 265 270
Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe
275 280 285
Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg
290 295 300
Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn Lys Glu
305 310 315 320
Met Ile Asn Asp Gly Ala Ser Trp Thr Ile Ile Ser Thr Asp Lys Ala
325 330 335
Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Leu Ala Pro Val Thr
340 345 350
Pro Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val
355 360 365
Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val
370 375 380
Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser
385 390 395 400
Met Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg
405 410 415
Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp
420 425 430
Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro
435 440 445
Gly Pro Arg Pro His Cys Ser Val Ala Gly Ala Ile Leu Pro Ala Asn
450 455 460
Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser
465 470 475 480
Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala
485 490 495
Thr Val Val Ser
500

<210> 149
<211> 1248
<212> DNA
<213> Homo Sapiens

<400> 149
caagatatcg aattccaaat ttgagggcct cccggctctg gcgccggagg gagagctcag 60
gccgccatgc gcgacaggac ccacgagctg agacaggggg atgacagctc ggacgaagag 120
gacaaggagc gggtcgcgct ggtggtgcac ccgggcacgg cacggctggg gagcccggac 180
gaggagttct tccacaaggt ccggacaatt cgtcagacta ttgtcaaact ggggaataaa 240
gtccaggagt tggagaaaca gcaggtcacc atcctggcca cgccccttcc cgaggagagc 300
atgaagcagg agctgcagaa cctgcgcgat gagatcaaac agctggggag ggagatccgc 360
ctgcagctga aggccataga gccccagaag gaggaagctg atgagaacta taactccgtc 420
aacacaagaa tgagaaaaac ccagcatggg gtcctgtccc agcaattcgt ggagctcatc 480
aacaagtgca attcaatgca gtccgaatac cgggagaaga acgtggagcg gattcggagg 540
cagctgaaga tcaccaatgc tggcatggtg tctgatgagg agttggatca gatgctggac 600
agtgggcaaa gcgaggtgtt tgtgtccaat atccttaagg acacgcaggt gactcgacag 660
gccttaaatg agatctcggc ccggcacagt gagatccagc agcttgaacg cagtattcgt 720
gagctgcacg acatattcac ttttctggct accgaagtgg agatgcaggg ggagatgatc 780

aatcggattg agaagaacat cctgagctca gcggactacg tggaacgtgg gcaggagcac 840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc 900
tgtgtgtcca tcaccgtcgt cctcctagca gtcatcattg gcgtcacagt ggttggataa 960
tgtcgcacat tgttggcact aggagcacca ggaacccagg gcctggcctt ctctcccagc 1020
agcctggggg gcaggcagag cctccagtcg gacccсttcc tcacacactg gcccctatgc 1080
agaagggcag acagttcttc tggggttggc agctgctcat tcatgatggc ctcctccttc 1140
aggcctcaat gcctgggga ggcctgcact gtcctgattg gccgggacac acggttttgt 1200
aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt 1248

<210> 150
<211> 297
<212> PRT
<213> Homo Sapiens

<400> 150
Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
1 5 10 15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
20 25 30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
35 40 45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
50 55 60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
65 70 75 80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
85 90 95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
100 105 110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
115 120 125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
130 135 140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
145 150 155 160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
165 170 175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
180 185 190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
195 200 205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
210 215 220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
225 230 235 240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
245 250 255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
260 265 270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
275 280 285
Val Ile Ile Gly Val Thr Val Val Gly
290 295

<210> 151

<211> 1953
<212> DNA
<213> Homo Sapiens

<400> 151
acgcctgcca ggagcaagcc gaagagccag ccggccggcg cactccgact ccgagcagtc 60
tctgtccttc gacccgagcc ccgcgccctt tccgggaccc ctgccccgcg ggcagcgctg 120
ccaacctgcc ggccatggag accccgtccc agcggcgcgc cacccgcagc ggggcgcagg 180
ccagctccac tccgctgtcg cccacccgca tcacccggct gcaggagaag gaggacctgc 240
aggagctcaa tgatcgcttg gcggtctaca tcgaccgtgt gcgctcgctg gaaacggaga 300
acgcagggct gcgccttcgc atcaccgagt ctgaagaggt ggtcagccgc gaggtgtccg 360
gcatcaaggc cgcctacgag gccgagctcg gggatgcccg caagaccctt gactcagtag 420
ccaaggagcg cgcccgcctg cagctggagc tgagcaaagt gcgtgaggag tttaaggagc 480
tgaaagcgcg caataccaag aaggagggtg acctgatagc tgctcaggct cggctgaagg 540
acctggaggc tctgctgaac tccaaggagg ccgcactgag cactgctctc agtgagaagc 600
gcacgctgga gggcgagctg catgatctgc ggggccaggt ggccaagctt gaggcagccc 660
taggtgaggc caagaagcaa cttcaggatg agatgctgcg gcgggtggat gctgagaaca 720
ggctgcagac catgaaggag gaactggact tccagaagaa catctacagt gaggagctgc 780
gtgagaccaa gcgccgtcat gagacccgac tggtggagat tgacaatggg aagcagcgtg 840
agtttgagag ccggctggcg gatgcgctgc aggaactgcg ggcccagcat gaggaccagg 900
tggagcagta taagaaggag ctggagaaga cttattctgc caagctggac aatgccaggc 960
agtctgctga gaggaacagc aacctggtgg gggctgccca cgaggagctg cagcagtcgc 1020
gcatccgcat cgacagcctc tctgcccagc tcagccagct ccagaagcag ctggcagcca 1080
aggaggcgaa gcttcgagac ctggaggact cactggcccg tgagcgggac accagccggc 1140
ggctgctggc ggaaaaggag cgggagatgg ccgagatgcg ggcaaggatg cagcagcagc 1200
tggacgagta ccaggagctt ctggacatca agctggccct ggacatggag atccacgcct 1260
accgcaagct cttggagggc gaggaggaga ggctacgcct gtcccccagc cctacctcgc 1320
agcgcagccg tggccgtgct tcctctcact catcccagac acagggtggg ggcagcgtca 1380
ccaaaaagcg caaactggag tccactgaga gccgcagcag cttctcacag cacgcacgca 1440
ctagcgggcg cgtggccgtg gaggaggtgg atgaggaggg caagtttgtc cggctgcgca 1500
acaagtccaa tgaggaccag tccatgggca attggcagat caagcgccag aatggagatg 1560
atcccttgct gacttaccgg ttcccaccaa agttcaccct gaaggctggg caggtggtga 1620
cgatctgggc tgcaggagct ggggccaccc acagcccccc taccgacctg gtgtggaagg 1680
cacagaacac ctggggctgc gggaacagcc tgcgtacggc tctcatcaac tccactgggg 1740
aagaagtggc catgcgcaag ctggtgcgct cagtgactgt ggttgaggac gacgaggatg 1800
aggatggaga tgacctgctc catcaccacc acgtgagtgg tagccgccgc tgaggccgag 1860
cctgcactgg ggccaccagc caggcctggg ggcagcctct ccccagcctc cccgtgccaa 1920
aaatcttttc attaaagaat gttttggaac ttt 1953

<210> 152
<211> 572
<212> PRT
<213> Homo Sapiens

<400> 152
Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
1 5 10 15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
20 25 30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
35 40 45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
50 55 60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65 70 75 80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
85 90 95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
100 105 110
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
115 120 125
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
130 135 140
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145 150 155 160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
165 170 175
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
180 185 190
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
195 200 205
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
210 215 220
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
225 230 235 240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
245 250 255
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
260 265 270
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
275 280 285
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
290 295 300
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
305 310 315 320
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
325 330 335
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
340 345 350
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
355 360 365
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
370 375 380
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
385 390 395 400
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
405 410 415
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
420 425 430
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
435 440 445
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
450 455 460
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
465 470 475 480
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
485 490 495
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
500 505 510
Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

```
        515                 520                 525
Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
    530                 535                 540
Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
545                 550                 555                 560
Leu Leu His His His His Val Ser Gly Ser Arg Arg
                565                 570
```

<210> 153
<211> 1610
<212> DNA
<213> Homo Sapiens

<400> 153

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ctgcaggaat tcggcacgag cggtcacgcc gagccagcgc ctgggcctgg aaccgggccg      60
tagccccccca gtttcgccca ccacctccct accatggacc cccgcaaagt gaacgagctt     120
cgggcctttg tgaaaatgtg taagcaggat ccgagcgttc tgtacaccga ggaaatgcgc     180
ttcctgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaagct     240
atatcagaag aaaataccaa ggaagaaaaa cctgatagta agaaggtgga ggaagactta     300
aaggcagacg aaccatcaag tgaggaaagt gatctagaaa ttgataaaga aggtgtgatt     360
gaaccagaca ctgatgctcc tcaagaaatg ggagatgaaa atgcggagat aacggaggag     420
atgatggatc aggcaaatga taaaaaagtg gctgctattg aagccctaaa tgatggtgaa     480
ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt     540
ttgtatgcca agagggccag tgtcttcgtc aaattacaga agccaaatgc tgccatccga     600
gactgtgaca gagccattga aataaatcct gattcagctc agccttacaa gtggcggggg     660
aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgcctgt     720
aaattggatt atgatgaaga tgctagtgca atgctgaaag aagttcaacc tagggcacag     780
aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa     840
agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagcccagag ggaggaagaa     900
gccagacgac agtcaggagc tcagtatggc tcttttccag gtggctttcc tgggggaatg     960
cctggtaatt ttcccggagg aatgcctgga atgggagggg gcatgcctgg aatggctgga    1020
atgcctggac tcaatgaaat tcttagtgat ccagaggttc ttgcagccat gcaggatcca    1080
gaagttatgg tggctttcca ggatgtggct cagaacccag caaatatgtc aaaataccag    1140
agcaacccaa aggttatgaa tctcatcagt aaattgtcag ccaaatttgg aggtcaagcg    1200
taatgtcctt ctgataaata aagcccttgc tgaaggaaaa gcaacctaga tcaccttatg    1260
gatgtcgcaa taatacaaac cagtgtacct ctgaccttct catcaagaga gctggggtgc    1320
tttgaagata atccctaccc ctctcccccca aatgcagctg aagcatttta cagtggtttg   1380
ccattagggt attcattcag ataatgtttt cctactagga attacaaact ttaaacactt    1440
tttaaatctt caaaatattt aaaacaaatt taaagggcct gttaattctt atatttttct    1500
ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg    1560
aagattactg ctctgagtga aataaaagtt attagtgcga ggcaaacata              1610
```

<210> 154
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 154

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Met Asp Pro Arg Lys Val Asn Glu Leu Arg Ala Phe Val Lys Met Cys
 1               5                  10                  15
Lys Gln Asp Pro Ser Val Leu Tyr Thr Glu Glu Met Arg Phe Leu Arg
            20                  25                  30
Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys
        35                  40                  45
Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys
```

```
    50                  55                  60
Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp
65                  70                  75                  80
Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro
                85                  90                  95
Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp
            100                 105                 110
Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly
        115                 120                 125
Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn
    130                 135                 140
Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys
145                 150                 155                 160
Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu
                165                 170                 175
Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His
            180                 185                 190
Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala
        195                 200                 205
Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val
    210                 215                 220
Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg
225                 230                 235                 240
Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys
                245                 250                 255
Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg
            260                 265                 270
Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly
        275                 280                 285
Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met
    290                 295                 300
Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro
305                 310                 315                 320
Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln
                325                 330                 335
Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro
            340                 345                 350
Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln
        355                 360                 365
Ala
```

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<210> 155
<211> 1323
<212> DNA
<213> Homo Sapiens

<400> 155
cacaaaggca ccaaaccaca aaacgtcaca cgtaaacatc atacgtggca accacaagcc      60
aatcagttgg atatttcatt cattggtata catatggact gtaaggtgtc tttcaggttg     120
cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc     180
tgtactttgc acaatcagag aatatagctg ctcatgagaa ttgtttgctg tattcttcag     240
gacttgtgga atgtgaggat caggatccac ttaatcctga tagaagtttt gatgtggaat     300
cagtaaagaa agaaatccag agaggaagga agttgaaatg caaattttgt cataaaagag     360
gagccaccgt gggatgtgat ttaaaaaact gtaacaagaa ttaccacttt ttctgtgcca     420
```

```
agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc      480
agcaacatgc tcaattcccg atcatcgctc aaagtgctaa attttcagga gtgaaaagaa      540
aaagaggaag gaagaaaccc ctctcaggca atcatgtaca gccacccgaa acaatgaaat      600
gtaatacatt cataagacaa gtgaaagaag agcatggcag acacacagat gcaactgtga      660
aagttccttt tcttaagaaa tgcaagggaa gcaggacttc ttaattactt acttgaagaa      720
atattagnca aagttcattc aattccagaa aaactcatgg atgagactta cttcagaatc      780
agactatgaa gaaatcggga gtgcactttt tgactgtaga ttgttcgaag acacatttgt      840
aaattttcaa gcagcaatag agaaaaaaat tcatgcatct caacaaaggt ggcagcagtt      900
gaaggaagag attgagctac ttcaggactt aaaacaaacc ttgtgctctt ttcaagaaaa      960
tagagatctt atgtcaagtt ctacatcaat atcatccctg tcttattagg gattaccatt     1020
tcctaagcca agagtcatgt caaattgcaa tcaggctcaa aaccagagac caggctgtga     1080
aatccacaca tctttagaac tagtcgtctc ctcttggcct cagcagctct tccctgttct     1140
tactggttga cattttgatc actctttgca cactcttgtg tttttgctc actgtcacac      1200
tcccagcacc tagtatgctc agtaaatgtt tgtggaataa gtgcataaaa tgttcttaac     1260
ctttgattct acttacagcc catgatagcc tcttagatat aataaatttg gattatacta     1320
aaa                                                                   1323
```

<210> 156
<211> 191
<212> PRT
<213> Homo Sapiens

<400> 156

```
Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
 1               5                  10                  15
Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
            20                  25                  30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
        35                  40                  45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
    50                  55                  60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65                  70                  75                  80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
                85                  90                  95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
            100                 105                 110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
        115                 120                 125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
    130                 135                 140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145                 150                 155                 160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
                165                 170                 175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
            180                 185                 190
```

<210> 157
<211> 4065
<212> DNA
<213> Homo Sapiens

<400> 157

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atgtcgactg gggacagttt tgagactcga tttgaaaaaa tggacaacct gctgcgggat       60
```

cccaaatcgg aagtgaattc ggattgtttg ctggatggat tggatgcttt ggtatatgat 120
ttggattttc ctgccttaag aaaaaacaaa aatattgaca actttttaag cagatataaa 180
gacacaataa ataaaatcag agatttacga atgaaagctg aagattatga agtagtgaag 240
gtgattggta gaggtgcatt tggagaagtt caattggtaa ggcataaatc caccaggaag 300
gtatatgcta tgaagcttct cagcaaattt gaaatgataa agagatctga ttctgctttt 360
ttctgggaag aaagggacat catggctttt gccaacagtc cttgggttgt tcagcttttt 420
tatgcattcc aagatgatcg ttatctctac atggtgatgg aatacatgcc tggtggagat 480
cttgtaaact taatgagcaa ctatgatgtg cctgaaaaat gggcacgatt ctatactgca 540
gaagtagttc ttgcattgga tgcaatccat tccatgggtt ttattcacag agatgtgaag 600
cctgataaca tgctgctgga taaatctgga catttgaagt tagcagattt tggtacttgt 660
atgaagatga ataaggaagg catggtacga tgtgatacag cggttggaac acctgattat 720
atttcccctg aagtattaaa atcccaaggt ggtgatggtt attatggaag agaatgtgac 780
tggtggtcgg ttggggtatt tttatacgaa atgcttgtag gtgatacacc tttttatgca 840
gattctttgg ttggaactta cagtaaaatt atgaaccata aaaattcact tacctttcct 900
gatgataatg acatatcaaa agaagcaaaa aaccttattt gtgccttcct tactgacagg 960
gaagtgaggt tagggcgaaa tggtgtagaa gaaatcaaac gacatctctt cttcaaaaat 1020
gaccagtggg cttgggaaac gctccgagac actgtagcac cagttgtacc cgatttaagt 1080
agtgacattg atactagtaa ttttgatgac ttggaagaag ataaaggaga ggaagaaaca 1140
ttccctattc ctaaagcttt cgttggcaat caactacctt ttgtaggatt tacatattat 1200
agcaatcgta gatacttatc ttcagcaaat cctaatgata acagaactag ctccaatgca 1260
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aatgaaatgc agttaaaaga tgaaatggag cagaagtgca gaacctcaaa cataaaacta 1380
gacaagataa tgaaagaatt ggatgaagag ggaaatcaaa gaagaaatct agaatctaca 1440
gtgtctcaga ttgagaagga gaaaatgttg ctacagcata gaattaatga gtaccaaaga 1500
aaagctgaac aggaaaatga gaagagaaga aatgtagaaa atgaagtttc tacattaaag 1560
gatcagttgg aagacttaaa gaaagtcagt cagaattcac agcttgctaa tgagaagctg 1620
tcccagttac aaaagcagct agaagaagcc aatgacttac ttaggacaga atcggacaca 1680
gctgtaagat tgaggaagag tcacacagag atgagcaagt caattagtca gttagagtcc 1740
ctgaacagag agttgcaaga gagaaatcga attttagaga attctaagtc acaaacagac 1800
aaagattatt accagctgca agctatatta gaagctgaac gaagagacag aggtcatgat 1860
tctgagatga ttggagacct tcaagctcga attacatctt tacaagagga ggtgaagcat 1920
ctcaaacata atctcgaaaa agtggaagga gaaagaaaag aggctcaaga catgcttaat 1980
cactcagaaa aggaaaagaa taatttagag atagatttaa actacaaact taaatcatta 2040
caacaacggt tagaacaaga ggtaaatgaa cacaaagtaa ccaaagctcg tttaactgac 2100
aaacatcaat ctattgaaga ggcaaagtct gtggcaatgt gtgagatgga aaaaaagctg 2160
aaagaagaaa gagaagctcg agagaaggct gaaaatcggg ttgttcagat tgagaaacag 2220
tgttccatgc tagacgttga tctgaagcaa tctcagcaga aactagaaca tttgactgga 2280
aataaagaaa ggatggagga tgaagttaag aatctaaccc tgcaactgga gcaggaatca 2340
aataagcggc tgttgttaca aaatgaattg aagactcaag catttgaggc agacaattta 2400
aaaggtttag aaaagcagat gaaacaggaa ataaatactt tattggaagc aaagagatta 2460
ttagaatttg agttagctca gcttacgaaa cagtatagag gaaatgaagg acagatgcgg 2520
gagctacaag atcagcttga agctgagcaa tatttctcga cactttataa aacccaggta 2580
aaggaactta aagaagaaat tgaagaaaaa aacagagaaa atttaaagaa aatacaggaa 2640
ctacaaaatg aaaaagaaac tcttgctact cagttggatc tagcagaaac aaaagctgag 2700
tctgagcagt tggcgcgagg ccttctggaa gaacagtatt ttgaattgac gcaagaaagc 2760
aagaaagctg cttcaagaaa tagacaagag attacagata aagatcacac tgttagtcgg 2820
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Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
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Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
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Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
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Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
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Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
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Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
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Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
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Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
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